



Title: "Isoforms of the Human Vitamin D Receptor" Inventor: Linda Anne Crofts Application No.: 09/509,482

(SEQ ID NO.15)-

Atty. Docket No. RICE-014

(SEQ ID NO.14)

Transcript 1: Transcript 6: MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPHR RAPLG STYLP PAPSG MEAMA ASTSL PDPGD FDRNV PRI DBD 477aa ← Transcript 9: (SEQ ID NO.16)



Inventor: Linda Anne Crofts Application No.: 09/509,482 Atty. Docket No. RICE-014

#### FIG. 4

- C. 5'...tgtttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA CGGTATTTTTACTCTTCATGTCTGAAAAGGCTATGATAA AGATCAAgtaagatatt...3' (SEQ ID NO: 6)

#### FIG. 5A

|                 |              | rig. JA      | <b>\</b>            |                   |
|-----------------|--------------|--------------|---------------------|-------------------|
| Transcrip       | t 6          |              |                     |                   |
| _               | Range: 1     | to 1463)     |                     |                   |
| _               | _            |              |                     |                   |
| 10              | 20           | 30           | 40                  | 50                |
| * *             | * *          | * *          | * *                 | * *               |
|                 |              | CGCCTTGGCA   |                     |                   |
| Caraggaaga      | AGACAGCCCC   | GCGGAACCGT   | ACCTCACCTC          | CTTATTCTTT        |
|                 |              | 1            | etGluTrpArg         | AsnLysLys>        |
|                 |              |              |                     |                   |
| 60              | 70           | 80           | 90                  | 100               |
| * *             | * *          | * *          | * *                 | * *               |
| ACCACCCA (IVII) | cccmcmccam   | GGTGCTCAGA   | NOTICO CONTRACTOR   | MOC1.001.100      |
|                 |              |              |                     |                   |
|                 |              | CCACGAGTCT   |                     | :                 |
| ArgSerAsp 1     | CrpLeuSerMet | : ValLeuArg  | ThrAlaGly V         | /alGluGluAla>     |
|                 |              |              |                     |                   |
| 110             | 120          | 130          | 140                 | 150               |
| * *             | * *          | * *          | * *                 | * *               |
| CTTTGGGTCT      | GAAGTGTCTG   | TGAGACCTCA   | CAGAAGAGCA          | CCCCTGGGCT        |
| GAAACCCAGA      | CTTCACAGAC   | ACTCTGGAGT   | GTCTTCTCGT          | GGGGACCCGA        |
|                 |              | /alArgProHis |                     |                   |
|                 | <b></b>      |              |                     |                   |
| 160             | 170          | 180          | 190                 | 200               |
| * *             | 1.0          | 100          | 190                 | 200               |
|                 |              |              |                     |                   |
|                 |              | CCTTCAGGGA   |                     |                   |
|                 |              | GGAAGTCCCT   |                     |                   |
| SerThrTyrLev    | 1 ProProAla  | ProserGly 1  | <b>detGluAlaMet</b> | : AlaAlaSer>      |
|                 |              |              |                     |                   |
| 210             | 220          | 230          | 240                 | 250               |
| * *             | * *          | * *          | * *                 | * *               |
| ACTTCCCTGC      | CTGACCCTGG   | AGACTTTGAC   | CGGAACGTGC          | CCCGGATCTG        |
| TGAAGGGACG      | GACTGGGACC   | TCTGAAACTG   | GCCTTGCACG          | GGGCCTAGAC        |
|                 |              |              |                     | ProArgIleCys>     |
|                 |              |              |                     | a dual gallong of |
| 260             | 270          | 280          | 290                 | 300               |
| 200             | 270          | 200          | 290                 | 300               |
|                 |              |              |                     |                   |
|                 |              | CCACTGGCTT   |                     |                   |
|                 |              | GGTGACCGAA   |                     |                   |
| GlyValCys       | GlyAspArg    | AlaThrGlyPho | e HisPheAsn         | AlaMetThr>        |
|                 |              |              |                     |                   |
| 310             | 320          | 330          | 340                 | 350               |
| * *             | * *          | * *          | * *                 | * *               |
| GTGAAGGCTG      | CAAAGGCTTC   | TTCAGGCGAA   | GCATGAAGCG          | GAAGGCACTA        |
|                 |              | AAGTCCGCTT   |                     |                   |
|                 |              |              |                     | g LysAlaLeu>      |
| -1 -armarkely   | - mleathing  | enaur Aur A  | -armanni put i      | a minuranda.      |
| 360             | 384          | 200          | 200                 | 400               |
| 360             | 370          | 380          | 390                 | 400               |
| T #             | ₩ ₩          | *            | # <b>*</b>          | ₩ ₩               |
|                 |              | GGACTGCCGC   |                     |                   |
| AAGTGGACGG      | GGAAGTTGCC   | CCTGACGGCG   | TAGTGGTTCC          | TGTTGGCTGC        |
| PheThrCys       | ProPheAsnG1  | y AspCysArg  | IleThrLys :         | AspAsnArgArg>     |
|                 |              |              |                     |                   |



450

440

# FIG. 5B

|   |                                      |           | 30       | 440         | 4        | 50               |
|---|--------------------------------------|-----------|----------|-------------|----------|------------------|
| 410   | 420                                  | _         |          | ± *         | *        | *                |
| * *   | * *                                  | *         | mama     | OT COC      | GGCATGAT | rga              |
| CCACTGCCAG G                                  | CTGCCGGC                             | TCAAACG   | org rere | CTCTAC      | CCGTACTI | <b>∖C</b> T      |
| CCACTGCCAG GC<br>GGTGACGGTC CC<br>HisCysGln A | GACGGCCG                             | AGTTTGC   | SAC ACAC | CIGINO      | GlyMetMe | et>              |
| GGTGACGGTC G                                  | lacvsArg                             | LeuLysAr  | gCys Va. | LASPITE     | 023      |                  |
| HisCysGin A                                   | 140,                                 |           |          | 400         |          | 500              |
| 460   | 470                                  |           | 480      | 490         | *        | *                |
| 460   |                                      | *         | *        | <b>x</b> -  |          | አጥC              |
| * * AGGAGTTCAT                                |                                      | CAGGAAG   | TGC AGA  | GGAAGCG     | GGAGATG  | MAC              |
| AGGAGTTCAT T                                  | CIGACAGAI                            | CTCCTTC   | ACG TCT  | CCTTCGC     | CCTCTAC  | TAG              |
| AGGAGTTCAT T                                  | AGACTGTCTA                           | 21.50117  | al GlnA  | rgLysAr     | g GluMet | :11e>            |
| TCCTCAAGTA L                                  | LeuThrAsp                            | ) GINGIA  | , a 1    | -           |          |                  |
| <b></b>                                       |                                      |           | 530      | 540         | )        | 550              |
| 510   | 520                                  |           |          |             | *        | *                |
| *   | *                                    | * *       |          | ~ አ ረጥርጥር፥( | GGCCCA   | AGCT             |
| CTGAAGCGGA<br>GACTTCGCCT                      | AGGAGGAGG                            | A GGCCTT  | GAAG GA  | CHCICIC     | CCGGGT   | TCGA             |
| CIGAAGCCC.                                    | TCCTCCTCC                            | T CCGGAA  | CTTC CT  | GTCAGAC.    | ArgProL  | vsLeu>           |
| GACTTCGCCT<br>LeuLysArg I                     | wsGluGluG                            | lu AlaLe  | uLys As  | bsernen     | Mr g     | -                |
| Leurysary .                                   | ,, 50                                |           |          |             | 0        | 600              |
| 560   | 57                                   | 10        | 580      | 59          | * *      | *                |
| 560   |                                      |           | *        | *           |          | ATA              |
| * * GTCTGAGGAG                                | as concce                            | TCATT     | GCCAT AC | TGCTGGA     | C GCCAC  | CT DT            |
| GTCTGAGGAG                                    | CAGCAGCG                             | or AGTAA  | CGGTA TO | BACGACCT    | G CGGGI  | -Uic>            |
| GTCTGAGGAG<br>CAGACTCCTC<br>SerGluGlu         | GTCGTCGC                             | a TleTle  | AlaIle   | LeuLeuAs    | SP ALAHI | Sura             |
| SerGluGlu                                     | GINGINAL                             | g 1102    |          |             |          | 650              |
|   |                                      |           | 630      | 64          | 40       | *                |
| 610   |                                      | 20        | *        | , <b>*</b>  | * *      |                  |
| * 1   |                                      | a mccci   | CTTCT G  | CCAGTTC     | CG GCCTC | CAGTI            |
| AGACCTACGA                                    | A CCCCACCI                           | AC TOCOL  | rcaaga C | GGTCAAG     | GC CGGAG | GTCAA            |
| AGACCTACGA<br>TCTGGATGC<br>LysThrTyrA         | r ggggtgg <i>i</i>                   | ATG AGGC  | Dhe Ci   | sGlnPhe     | Arg Prol | eroVa1>          |
| LysThrTyrA                                    | sp ProThri                           | ryr SerA  | spric vi | _           |          |                  |
| -2  |                                      |           | 680      | $\epsilon$  | 90       | 700              |
| 66  | 1.2                                  | 670       |          | *           | *        | * *              |
| *   | * *                                  | *         |          | mccxccc     | CA ACTC  | CAGACA           |
|   | * *  G ATGGTGG  AC TACCACO           | AGG GAGC  | CATCCT   | TCCAGGC     | GGT TGAG | GTCTGT           |
| CGIGIOM                                       | AC TACCACO                           | TCC CTCG  | GTAGGA   | AGGICCG     | ×o AsnSe | rArgHis>         |
| GCACACIII                                     | AspGlvG]                             | yGly Ser  | HisPro   | Serarge     | 10 11000 |                  |
| Argvalasi                                     | [ Nober]                             | -         |          |             | 740      | 750              |
| -   | 10                                   | 720       | 730      |             | 740      | * *              |
|   | 10                                   |           | * *      | *           |          | ол <i>от</i> СТА |
| *   | GC TTCTCT                            | cccc ACT  | CCTCCTC  | CTCCTGC     | TCA GAT  | CMC1C1.          |
| CACTCCCA                                      | GC TICICI                            | CCCC TGA  | GGAGGAG  | GAGGAC      | BAGT CTA | GIGACA1          |
| GTGAGGGT                                      | GC TTCTCT<br>CG AAGAGA<br>Ser PheSer | COLC TON  | erserse  | r SerCy     | sSer Asp | HISCAP           |
| ThrProS                                       | er Pheser                            | GIA Wabe  | ,02000   |             |          |                  |
|   |                                      |           | 780      |             | 790      | 000              |
| •   | 760                                  | 770       |          |             | *        | •                |
| *   | TTC AGACA                            | ×<br>     |          | GCTTCT      | CCAA TCT | rggatche         |
| TCACCTC                                       | TTC AGACA'                           | rgatg ga  | CICGICC: | r CGAAGA    | GGTT AG  | ACCTAGAC         |
| дстсса  | AAG TCTGT                            | ACTAC CT  | GAGCAGG. | corPhes     | erAsn L  | euAspLeu>        |
| TIETHYSE                                      | AAG TCTGT<br>rSer AspM               | etMet As  | pserser  | 3611        |          |                  |
| TTC1111                                       |                                      |           |          |             | 840      | <b>0</b> -       |
|   | 810                                  | 820       | 83       | . •         | *        | * *              |
| •   | * *                                  | *         | *        | *           | AGAGC TO | TCCCAGCT         |
| - amak ki                                     | GAAG ATTC                            | AGATGA CO | CTTCTGI  | G ACCCT     | mones ac | AGGGTCGA         |
| AGTGAA  | COUNC TARG                           | CTACT G   | GGAAGAC? | AC TGGGA    | LOIN LO  | SerGlnLeu>       |
| TCAC'I'I                                      | oli yençe                            | raspasp   | proSerVa | al ThrLe    | MOIN DE  | ıSerGlnLeu>      |
| SerGlu  | GIR Wahne                            |           |          |             |          |                  |
|   |                                      |           |          |             |          |                  |
|   |                                      |           |          |             |          |                  |

# FIG. 5C

| 860  | 870   | 880   | 890   | 900  |
|--|---|---|---|--|
| * *  | * *   | * *   | * *   | * *  |
| CUCCAUCCUC   | CCCCACCTGG  | CMC V CCMCCM  | CACTTACACC  | 74CC7 7 7 7 7 CC   |
|  |   |   |   |  |
|  | GGGGTGGACC  |   |   |  |
| SerMetLeu  | ProHisLeu A   | AlaAspLeuVal  | l SerTyrSer   | IleGlnLys>   |
|  |   |   |   |  |
| 910  | 920   | 930   | 940   | 950  |
| * *  | * *   | * *   | * *   | * *  |
| max mmaaamm  |   |   |   |  |
|  | TGCTAAGATG  |   |   |  |
| AGTAACCGAA   | ACGATTCTAC  | TATGGTCCTA  | AGTCTCTGGA  | GTGGAGACTC   |
| ValIleGlyPho   | a AlaLysMet   | IleProGly I   | PheArgAspLe   | ThrSerGlu>   |
| <del>-</del>   | -   | _   |   |  |
| 960  | 970   | 980   | 990   | 1000   |
| * *  | * *   |   |   | = =  |
|  |   |   | * *   | * *  |
| GACCAGATCG   | TACTGCTGAA  | GTCAAGTGCC  | ATTGAGGTCA  | TCATGTTGCG   |
| CTGGTCTAGC   | ATGACGACTT  | CAGTTCACGG  | TAACTCCAGT  | AGTACAACGC   |
|  |   |   |   | [leMetLeuArg>  |
|  | · u + D c u D c u D j .   | Derbernie   | 110010101   | - Tonce Deaning  |
| 4004   |   | 4 A = -   | 444   |  |
| 1010   | 1020  | 1030  | 1040  | 1050   |
| * *  | * *   | * *   | * *   | * *  |
| CTCCAATGAG   | TCCTTCACCA  | TGGACGACAT  | GTCCTGGACC  | TGTGGCAACC   |
| GAGGTTACTC   | AGGAAGTGGT  | ACCTGCTGTA  | CAGGACCTGG  | ACACCGTTGG   |
|  | SerPheThr N   |   |   |  |
| SelAshGlu  | serphernr r   | Metaspaspme   | . serripini   | CysGlyAsn>   |
|  |   |   |   |  |
| 1060   | 1070  | 1080  | 1090  | 1100   |
| * *  | * *   | * *   | * *   | * *  |
| AAGACTACAA   | GTACCGCGTC  | AGTGACGTGA  | CCAAAGCCGG  | ACACAGCCTG   |
|  |   |   |   |  |
| ጥጥር ጥር ልምን መመር ነው  | CATGGCGCAG  |   |   |  |
|  | CATGGCGCAG  | TCACTGCACT  | GGTTTCGGCC  | TGTGTCGGAC   |
|  |   | TCACTGCACT  | GGTTTCGGCC  |  |
|  |   | TCACTGCACT  | GGTTTCGGCC  | TGTGTCGGAC / HisSerLeu>  |
|  |   | TCACTGCACT  | GGTTTCGGCC  | TGTGTCGGAC   |
| GlnAspTyrLy  | s TyrArgVal   | TCACTGCACT<br>SerAspVal   | GGTTTCGGCC<br>ChrLysAlaGl   | TGTGTCGGAC / HisSerLeu>  |
| GlnAspTyrLy: 1110 *  | TyrArgVal   | TCACTGCACT<br>SerAspVal 1   | GGTTTCGGCC<br>ThrLysAlaGly<br>1140<br>* *   | TGTGTCGGAC / HisSerLeu> 1150 * *   |
| GlnAspTyrLy: 1110  * * GAGCTGATTG  | TyrArgVal  1120  *  AGCCCCTCAT  | TCACTGCACT SerAspVal 1 1130   | GGTTTCGGCC<br>ThrLysAlaGly<br>1140<br>* *<br>GTGGGACTGA   | TGTGTCGGAC HisSerLeu> 1150 * AGAAGCTGAA  |
| GlnAspTyrLy:  1110  *  GAGCTGATTG  CTCGACTAAC  | TyrArgVal  1120  *  AGCCCCTCAT TCGGGGAGTA   | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC  | GGTTTCGGCC PhrLysAlaGly 1140 * * GTGGGACTGA CACCCTGACT  | TGTGTCGGAC HisSerLeu> 1150 * AGAAGCTGAA TCTTCGACTT   |
| GlnAspTyrLy:  1110  *  GAGCTGATTG  CTCGACTAAC  | TyrArgVal  1120  *  AGCCCCTCAT TCGGGGAGTA   | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC  | GGTTTCGGCC PhrLysAlaGly 1140 * * GTGGGACTGA CACCCTGACT  | TGTGTCGGAC HisSerLeu> 1150 * AGAAGCTGAA  |
| GlnAspTyrLy:  1110  *  GAGCTGATTG  CTCGACTAAC  | TyrArgVal  1120  *  AGCCCCTCAT TCGGGGAGTA   | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC  | GGTTTCGGCC PhrLysAlaGly 1140 * * GTGGGACTGA CACCCTGACT  | TGTGTCGGAC HisSerLeu> 1150 * AGAAGCTGAA TCTTCGACTT   |
| GlnAspTyrLy:  1110  *  GAGCTGATTG  CTCGACTAAC  GluLeulle   | TyrArgVal  1120  *  AGCCCCTCAT  TCGGGGAGTA  GluProLeuIl   | TCACTGCACT SerAspVal 1130  * * CAAGTTCCAG GTTCAAGGTC e LysPheGln  | GGTTTCGGCC ThrLysAlaGly 1140  * * GTGGGACTGA CACCCTGACT ValGlyLeu   | TGTGTCGGAC HisSerLeu>  1150  * AGAAGCTGAA TCTTCGACTT LysLysLeuAsn>   |
| GlnAspTyrLy:  1110  *  GAGCTGATTG  CTCGACTAAC  | TyrArgVal  1120  *  AGCCCCTCAT TCGGGGAGTA   | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC  | GGTTTCGGCC PhrLysAlaGly 1140 * * GTGGGACTGA CACCCTGACT  | TGTGTCGGAC HisSerLeu> 1150 * AGAAGCTGAA TCTTCGACTT   |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  | TYPATGVal  1120  *  AGCCCCTCAT  TCGGGGAGTA GluProLeuIle  1170  *  *   | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC e LysPheGln 1180 * *   | GGTTTCGGCC ThrLysAlaGly  1140  *  GTGGGACTGA CACCCTGACT ValGlyLeu  1190  *  *   | TGTGTCGAC THISSERLEU>  1150 * AGAAGCTGAA TCTTCGACTT LysLysLeuAsn> 1200 * *   |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG  | AGCCCCTCAT TCGGGGAGTA GluProLeuIle  1170  * GAGGAGCATG  | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC e LysPheGln 1180  * * TCCTGCTCAT   | GGTTTCGGCC ThrLysAlaGly  1140  *  GTGGGACTGA CACCCTGACT ValGlyLeu  1190  *  GGCCATCTGC  | TGTGTCGGAC HisSerLeu>  1150  * AGAAGCTGAA TCTTCGACTT LysLysLeuAsn>  1200  * ATCGTCTCCC   |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG  | TYPATGVal  1120  *  AGCCCCTCAT  TCGGGGAGTA GluProLeuIle  1170  *  *   | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC e LysPheGln 1180  * * TCCTGCTCAT   | GGTTTCGGCC ThrLysAlaGly  1140  *  GTGGGACTGA CACCCTGACT ValGlyLeu  1190  *  GGCCATCTGC  | TGTGTCGGAC HisSerLeu>  1150  * AGAAGCTGAA TCTTCGACTT LysLysLeuAsn>  1200  * ATCGTCTCCC   |
| GlnAspTyrLy:  1110  * GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * CTTGCATGAG GAACGTACTC   | AGCCCCTCAT TCGGGGAGTA GluProLeuIle  1170  * GAGGAGCATG  | TCACTGCACT SerAspVal 3  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA  | GGTTTCGCC ThrLysAlaGly  1140  *  GTGGGACTGA CACCCTGACT ValGlyLeu  1190  *  GGCCATCTGC CCGGTAGACG  | TGTGTCGGAC THISSETLEU>  1150 * AGAAGCTGAA TCTTCGACTT LysLysLeuAsn> 1200 * ATCGTCTCCC TAGCAGAGGG  |
| GlnAspTyrLy:  1110  * GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * CTTGCATGAG GAACGTACTC   | AGCCCCTCAT TCGGGGAGTA GluProLeuIl  1170  * GAGGAGCATG CTCCTCGTAC  | TCACTGCACT SerAspVal 3  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA  | GGTTTCGCC ThrLysAlaGly  1140  *  GTGGGACTGA CACCCTGACT ValGlyLeu  1190  *  GGCCATCTGC CCGGTAGACG  | TGTGTCGGAC THISSETLEU>  1150 * AGAAGCTGAA TCTTCGACTT LysLysLeuAsn> 1200 * ATCGTCTCCC TAGCAGAGGG  |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu   | AGCCCCTCAT TCGGGGAGTA GluProLeuIl  GAGGAGCATG CTCCTCGTAC GluGluHis  | TCACTGCACT SerAspVal 7 1130  * * CAAGTTCCAG GTTCAAGGTC e LysPheGln 1180  * * TCCTGCTCAT AGGACGAGTA ValLeuLeuMer   | GGTTTCGGCC ThrLysAlaGly  1140  * GTGGGACTGA CACCCTGACT ValGlyLeu  1190  * GGCCATCTGC CCGGTAGACG   | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210   | AGCCCCTCAT TCGGGGAGTA GluProLeuIl  GAGGAGCATG CTCCTCGTAC GluGluHis  | TCACTGCACT SerAspVal 7  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA ValLeuLeuMed   | GGTTTCGGCC ThrLysAlaGly  1140  * * GTGGGACTGA CACCCTGACT ValGlyLeu 1  1190  * * GGCCATCTGC CCGGTAGACG E AlaIleCys   | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  * *  | AGCCCCTCAT TCGGGGAGTA GluProLeuIle  1170  * GAGGAGCATG CTCCTCGTAC GluGluHis 1220  *   | TCACTGCACT SerAspVal 7  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA ValLeuLeuMed  1230  * *  | GGTTTCGGCC ThrLysAlaGly  1140  * *  GTGGGACTGA CACCCTGACT ValGlyLeu 1  1190  * *  GGCCATCTGC CCGGTAGACG E AlaIleCys  1240  * *  | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  *  *   |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  *  CAGATCGTCC  | TyrArgVal  1120  *  AGCCCCTCAT  TCGGGGAGTA  GluProLeuIl  1170  *  GAGGAGCATG  CTCCTCGTAC  GluGluHis  1220  *  TGGGGTGCAG  | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC e LysPheGln 1180  * * TCCTGCTCAT AGGACGAGTA ValLeuLeuMet 1230  * * GACGCCGCGC  | GGTTTCGGCC ThrLysAlaGly  1140  * * GTGGGACTGA CACCCTGACT ValGlyLeu  1190  * * GGCCATCTGC CCGGTAGACG CCGGTAGACG E AlaIleCys  1240  * * TGATTGAGGC  | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  *  CATCCAGGAC                                       |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  *  CAGATCGTCC  | AGCCCCTCAT TCGGGGAGTA GluProLeuIle  1170  * GAGGAGCATG CTCCTCGTAC GluGluHis 1220  *   | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC e LysPheGln 1180  * * TCCTGCTCAT AGGACGAGTA ValLeuLeuMet 1230  * * GACGCCGCGC  | GGTTTCGGCC ThrLysAlaGly  1140  * * GTGGGACTGA CACCCTGACT ValGlyLeu  1190  * * GGCCATCTGC CCGGTAGACG CCGGTAGACG E AlaIleCys  1240  * * TGATTGAGGC  | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  *  CATCCAGGAC                                       |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  *  CAGATCGTCC GTCTAGCAGG   | TYPATGVal  1120  *  AGCCCTCAT  TCGGGGAGTA  GluProLeuIl  1170  *  GAGGAGCATG  CTCCTCGTAC  GluGluHis  1220  *  TGGGGTGCAG  ACCCCACGTC                                     | TCACTGCACT SerAspVal 7  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA ValLeuLeuMer  1230  *  GACGCCGCGC CTGCGGCGCGC  | GGTTTCGCC ThrLysAlaGly 1140  * * GTGGGACTGA CACCCTGACT ValGlyLeu 1 1190  * * GGCCATCTGC CCGGTAGACG E AlaIleCys 1240  * TGATTGAGGC ACTAACTCCG  | TGTGTCGGAC HisSerLeu>  1150  *  AGAAGCTGAA TCTTCGACTT LysLysLeuAsn>  1200  *  ATCGTCTCCC TAGCAGAGGG IleValSer>  1250  *  CATCCAGGAC GTAGGTCCTG                                 |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  *  CAGATCGTCC GTCTAGCAGG   | TYPATGVal  1120  *  AGCCCCTCAT  TCGGGGAGTA  GluProLeuIl  1170  *  GAGGAGCATG  CTCCTCGTAC  GluGluHis  1220  *  TGGGGTGCAG  ACCCCACGTC                                    | TCACTGCACT SerAspVal 7  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA ValLeuLeuMer  1230  *  GACGCCGCGC CTGCGGCGCGC  | GGTTTCGCC ThrLysAlaGly 1140  * * GTGGGACTGA CACCCTGACT ValGlyLeu 1 1190  * * GGCCATCTGC CCGGTAGACG E AlaIleCys 1240  * TGATTGAGGC ACTAACTCCG  | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  *  CATCCAGGAC                                       |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  *  CAGATCGTCC GTCTAGCAGG   | TYPATGVal  1120  *  AGCCCCTCAT  TCGGGGAGTA  GluProLeuIl  1170  *  GAGGAGCATG  CTCCTCGTAC  GluGluHis  1220  *  TGGGGTGCAG  ACCCCACGTC                                    | TCACTGCACT SerAspVal 7  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA ValLeuLeuMer  1230  *  GACGCCGCGC CTGCGGCGCGC  | GGTTTCGCC ThrLysAlaGly 1140  * * GTGGGACTGA CACCCTGACT ValGlyLeu 1 1190  * * GGCCATCTGC CCGGTAGACG E AlaIleCys 1240  * TGATTGAGGC ACTAACTCCG  | TGTGTCGGAC HisSerLeu>  1150  *  AGAAGCTGAA TCTTCGACTT LysLysLeuAsn>  1200  *  ATCGTCTCCC TAGCAGAGGG IleValSer>  1250  *  CATCCAGGAC GTAGGTCCTG                                 |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  * *  CAGATCGTCC GTCTAGCAGG ProAspArgPr                               | AGCCCCTCAT TCGGGGAGTA GluProLeuIl  GAGGAGCATG CTCCTCGTAC GluGluHis  1220  * TGGGGTGCAG ACCCCACGTC o GlyValGln   | TCACTGCACT SerAspVal 7  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA ValLeuLeuMed  1230  * *  GACGCCGCGC CTGCGGCGCG AspAlaAla                               | GGTTTCGGCC ThrLysAlaGly  1140  * *  GTGGGACTGA CACCCTGACT ValGlyLeu 1  1190  * *  GGCCATCTGC CCGGTAGACG E AlaIleCys  1240  * TGATTGAGGC ACTAACTCCG LeuIleGluAla   | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  *  CATCCAGGAC  GTAGGTCCTG  a IleGlnAsp>             |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  *  CAGATCGTCC GTCTAGCAGG   | AGCCCCTCAT TCGGGGAGTA GluProLeuIl  GAGGAGCATG CTCCTCGTAC GluGluHis  1220  * TGGGGTGCAG ACCCCACGTC o GlyValGln   | TCACTGCACT SerAspVal 7  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA ValLeuLeuMer  1230  *  GACGCCGCGC CTGCGGCGCGC  | GGTTTCGCC ThrLysAlaGly 1140  * * GTGGGACTGA CACCCTGACT ValGlyLeu 1 1190  * * GGCCATCTGC CCGGTAGACG E AlaIleCys 1240  * TGATTGAGGC ACTAACTCCG  | TGTGTCGGAC HisSerLeu>  1150  *  AGAAGCTGAA TCTTCGACTT LysLysLeuAsn>  1200  *  ATCGTCTCCC TAGCAGAGGG IleValSer>  1250  *  CATCCAGGAC GTAGGTCCTG                                 |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  * *  CAGATCGTCC GTCTAGCAGG ProAspArgPr                               | AGCCCCTCAT TCGGGGAGTA GluProLeuIl  GAGGAGCATG CTCCTCGTAC GluGluHis  1220  * TGGGGTGCAG ACCCCACGTC o GlyValGln   | TCACTGCACT SerAspVal 7  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA ValLeuLeuMed  1230  * *  GACGCCGCGC CTGCGGCGCG AspAlaAla                               | GGTTTCGGCC ThrLysAlaGly  1140  * *  GTGGGACTGA CACCCTGACT ValGlyLeu 1  1190  * *  GGCCATCTGC CCGGTAGACG E AlaIleCys  1240  * TGATTGAGGC ACTAACTCCG LeuIleGluAla   | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  *  CATCCAGGAC  GTAGGTCCTG  a IleGlnAsp>             |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  * *  CAGATCGTCC GTCTAGCAGG ProAspArgPr  1260  * *                    | TyrargVal  1120  * * * * * * * * * * * * * * * * * *  | TCACTGCACT SerAspVal  1130  * CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * TCCTGCTCAT AGGACGAGTA ValLeuLeuMe  1230  * GACGCCGCGC CTGCGGCGCG AspAlaAla  1280  *                                  | GGTTTCGGCC ThrLysAlaGly  1140  * *  GTGGGACTGA CACCCTGACT ValGlyLeu 1  1190  * *  GGCCATCTGC CCGGTAGACG CAGGTAGACG ALAILeCys  1240  * TGATTGAGGC ACTAACTCCG LeuIleGluAla  1290  * *                           | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  *  CATCCAGGAC  GTAGGTCCTG  A IleGlnAsp>  1300  *  * |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  * *  CAGATCGTCC GTCTAGCAGG ProAspArgPr  1260  *  CGCCTGTCCA          | TyrargVal  1120  *  AGCCCCTCAT  TCGGGGAGTA  GluProLeuIle  1170  *  GAGGAGCATG  CTCCTCGTAC  GluGluHis  1220  *  TGGGGTGCAG  ACCCCACGTC  O GlyValGln  1270  *  ACACACTGCA | TCACTGCACT SerAspVal 1 1130  * * CAAGTTCCAG GTTCAAGGTC e LysPheGln 1180  * * TCCTGCTCAT AGGACGAGTA ValLeuLeuMe 1230  * * GACGCCGCGC CTGCGGCGCG CTGCGGCGCG AspAlaAla 1280  * * GACGTACATC      | GGTTTCGGCC ThrLysAlaGly  1140  * *  GTGGGACTGA CACCCTGACT ValGlyLeu  1190  * *  GGCCATCTGC CCGGTAGACG CAGGTAGACG ALALLECYS  1240  * *  TGATTGAGGC ACTAACTCCG LeuileGluAla  1290  * *  CGCTGCCGCC              | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  *  CATCCAGGAC  GTAGGTCCTG  a IleGlnAsp>  ACCCGCCCCC |
| GlnAspTyrLy:  1110  * *  GAGCTGATTG CTCGACTAAC GluLeuIle  1160  * *  CTTGCATGAG GAACGTACTC LeuHisGlu  1210  *  CAGATCGTCC GTCTAGCAGG ProAspArgPr  1260  *  CGCCTGTCCA GCGGACAGGT | ACACACTGCA TTYRATGVAL  1120  * * * * * * * * * * * * * * * * * *  | TCACTGCACT SerAspVal 1  1130  * *  CAAGTTCCAG GTTCAAGGTC e LysPheGln  1180  * *  TCCTGCTCAT AGGACGAGTA ValLeuLeuMet  1230  *  GACGCCGCGC CTGCGGCGCG AspAlaAla  1280  *  GACGTACATC CTGCATGTAG | GGTTTCGGCC ThrLysAlaGly  1140  * *  GTGGGACTGA CACCCTGACT ValGlyLeu  1190  * *  GGCCATCTGC CCGGTAGACG CCGGTAGACG E AlaIleCys  1240  * *  TGATTGAGGC ACTAACTCCG LeuIleGluAla  1290  * *  CGCTGCCGCC GCGACGGCGG | TGTGTCGGAC  HisSerLeu>  1150  *  AGAAGCTGAA  TCTTCGACTT  LysLysLeuAsn>  1200  *  ATCGTCTCCC  TAGCAGAGGG  IleValSer>  1250  *  CATCCAGGAC  GTAGGTCCTG  a IleGlnAsp>  ACCCGCCCCC |

#### FIG. 5D

1310 1320 1330 1340 1350 GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu> 1360 1370 1380 1390 GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln> 1410 1420 1430 1440 1450 CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA GGACTCACGT CGTACTTCGA TTGCGGGGGAA CACGAGCTTC ACAAACCGTT ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn> 1460

TGAGATCTCC TGA (SEQ ID NO:2)
ACTCTAGAGG ACT (SEQ ID NO:17)
GluIleSer \*\*\*>(SEQ ID NO:9)



### FIG. 6A

|              |                | 1 10.07      | •                    |                |
|--------------|----------------|--------------|----------------------|----------------|
| Transcrip    | t 9            |              |                      |                |
| (Sequence    | range: 1       | to 1382)     |                      |                |
| 10           | 20             | 30           | 40                   | 50             |
| * *          | * *            | * *          | * *                  | * *            |
| OMMBOO BOOM  |                |              |                      |                |
|              |                |              | TGGAGTGGAG           |                |
| CAAAGGAAGA   | AGACAGCCCC     | GCGGAACCGT   | ACCTCACCTC           | CTTATTCTTT     |
|              |                |              | <b>letGluTrpAr</b> q | AsnLysLys>     |
|              |                |              |                      |                |
| 60           | 70             | 80           | 90                   | 100            |
| * *          | * *            | * *          | * *                  | * *            |
| AGGAGCGATT   | GGCTGTCGAT     | GGTGCTCAGA   | ACTGCTGGAG           | TGGAGGGGAT     |
|              |                |              | TGACGACCTC           |                |
|              |                |              |                      | /alGluGlyMet>  |
| .mgocr.nop 1 | . I pacabeline | - varieumig  | IIII NEGGE           | arordorymety   |
| 110          | 120            | 130          | 140                  | 150            |
| 110          | * *            | 130          | 140                  | 130            |
| 0010001100   |                |              |                      |                |
|              |                |              | TGACCCTGGA           |                |
|              |                |              | ACTGGGACCT           |                |
| GluAlaMet    | AlaAlaSer '    | ThrSerLeuPro | AspProGly            | AspPheAsp>     |
|              |                |              |                      |                |
| 160          | 170            | 180          | 190                  | 200            |
| * *          | * *            | * *          | * *                  | * *            |
|              |                |              | GAGACCGAGC           |                |
| CCTTGCACGG   | GGCCTAGACA     | CCCCACACAC   | CTCTGGCTCG           | GTGACCGAAA     |
| ArgAsnValPro | ArgIleCys      | GlyValCys (  | GlyAspArgAla         | ThrGlyPhe>     |
|              |                | •            |                      |                |
| 210          | 220            | 230          | 240                  | 250            |
| * *          | * *            | * *          | * *                  | * *            |
| CACTTCAATG   | СТАТСАССТС     | TGAAGGCTGC   | AAAGGCTTCT           | TCAGGCGAAG     |
|              |                |              | TTTCCGAAGA           |                |
|              |                |              |                      | PheArgArgSer>  |
| HISPHEASH A  | tamecinicy:    | s Gludlycys  | DysGIyFile i         | menightyset>   |
| 260          | 272            | 200          |                      | 200            |
| 260          | 270            | 280          | 290                  | 300            |
| <b>#</b> #   | * *            | * *          | * *                  | * *            |
|              |                |              | CTTCAACGGG           |                |
|              |                |              | GAAGTTGCCC           |                |
| MetLysArg    | LysAlaLeu      | PheThrCysPro | o PheAsnGly          | AspCysArg>     |
|              |                | •            |                      |                |
| 310          | 320            | 330          | 340                  | 350            |
| * *          | * *            | * *          | * *                  | * *            |
| TCACCAAGGA   | CAACCGACGC     | CACTGCCAGG   | CCTGCCGGCT           | CAAACGCTGT     |
| AGTGGTTCCT   | GTTGGCTGCG     | GTGACGGTCC   | GGACGGCCGA           | GTTTGCGACA     |
|              |                |              |                      | LysArgCys>     |
|              |                |              |                      | -2 3 -2        |
| 360          | 370            | 380          | 390                  | 400            |
| * *          | * *            |              |                      | * *            |
| GTGGACATCG   | GCATGATGAA     | CCACጥጥC Aጥጥ  | CTGACAGATG           | AGGA AGTGCA    |
|              |                |              | GACTGTCTAC           |                |
|              |                |              |                      | GluGluValGln>  |
| ACTUSPITE (  | этумесмеспу    | a Grasmerre  | menturab (           | ernern Agreru> |

# FIG. 6B

|   | FIG. 6       | В             |                 |               |
|---|--------------|---------------|-----------------|---------------|
|   |              | _             | 440             | 450           |
| 410 42  | 0 43         | _             | * *             | *             |
| * * * GAGGAAGCGG GAGATGATC                                  | * "<br>      | A GGAGGAG     | GAG GCCTTG      | AAGG          |
| GAGGAAGCGG GAGATGATC CTCCTTCGCC CTCTACTAG                   | C JGAAGCGCCI | T CCTCCT      | CCTC CGGAAC     | TTCC          |
| CTCCTTCGCC CTCTACTAC ArgLysArg GluMetile                    | G ACTICGOO   | ys GluGl      | uGlu AlaLev     | ılys>         |
| ArgLysArg GluMetlle   | Feary or - 2 | -             |                 |               |
|   |              |               |                 | 500           |
| 460 4   | 70 4         | в0            | 490             | *             |
|   |              | * *           | ·<br>ጉርአጥ ርልጥፕG | CCATA         |
| ACAGTCTGCG GCCCAAGC   | TG TCTGAGGA  | GC AGCAGC     | COCHA CTAAC     | GGTAT         |
| ACAGTCTGCG GCCCAAGC<br>TGTCAGACGC CGGGTTCG                  | AC AGACTCCT  | CG TCGTCC     | Aratle TleA     | laIle>        |
| TGTCAGACGC CGGGTTCG<br>AspSerLeuArg ProLysL                 | eu SerGluGl  | u Gingin      | AIGIIC          |               |
| Aspserbeaus   |              |               |                 |               |
|   |              | - 3 0         | 540             | 550           |
|   | 320          | 530<br>* *    | *               | * *           |
| * * * CTGCTGGACG CCCACCA                                    | * ~ ~        | CAC CCCAC     | CTACT CCGA      | CTTCTG        |
| CTGCTGGACG CCCACCA  | TAA GACCIAC  | CTG GGGTG     | GATGA GGCT      | GAAGAC        |
| CTGCTGGACG CCCACCA<br>GACGACCTGC GGGTGGT                    | ATT CIGGAIC  | Asp ProTh     | arTyr SerAs     | pPheCys>      |
| GACGACCTGC GGGTGGT<br>LeuLeuAsp AlaHisHi                    | suys IIII-I  |               |                 | 600           |
|   | 570          | 580           | 590             | * *           |
| 560   |              | *             | * * *           | TATCCTT       |
| CCAGTTCCGG CCTCCAG  | GTTC GTGTGA  | ATGA TGGT     | GGAGGG AGC      | GTAGGAA       |
| CCAGTTCCGG CCTCCAC<br>GGTCAAGGCC GGAGGT                     | CAAG CACACT  | TACT ACCA     | CUTCUC FOR      | HisPro>       |
| GGTCAAGGCC GGAGGT<br>GlnPheArg ProPro                       | Val ArgValA  | snAsp Gry     | /G13013 -       |               |
| Gillellering  |              | 630           | 640             | 650           |
| 610   | 620          |               | * *             | * *           |
| CCAGGCCCAA CTCCAC   | *<br>አርጥርር(  | AGCT TCT      | CTGGGGA CTC     | CTCCTCC       |
| CCAGGCCCAA CTCCAC   | SACAC ACICO  | TCGA AGA      | GACCCCT GAC     | GAGGAGG       |
| CCAGGCCCAA CTCCAC<br>GGTCCGGGTT GAGGTC<br>SerArgProAsn SerA | -cuis ThrPr  | Ser Phes      | erGlyAsp So     | arserser      |
| SerArgProAsn SerA   | rgnis in     |               |                 | 700           |
|   | 670          | 680           | 690<br>• *      | * *           |
| 660   |              | *             |                 | TCGTCCAG      |
| TCCTGCTCAG ATCAC  | TGTAT CACCI  | CTTCA GAG     | CATGATGG AC     | AGCAGGTC      |
| AGGACGAGTC TAGTO<br>SerCysSer AspHi:                        | TGTAT CACCT  | GAAGT CT      | GIACIACO I      | SerSerSer>    |
| AGGACGACTO  | SCyslle Thr  | SerSer As     | bMechec 1001    | <del>,</del>  |
| Sercysbor   |              | 730           | 740             | 750           |
| 710   | 720          |               | * *             | * *           |
| * * CTTCTCCAAT CTGG   | * *          | NONDER TO     | CAGATGAC C      | CTTCTGTGA     |
| CTTCTCCAAT CTGG   | ATCTGA GIGA  | MCMMCM A      | AGTCTACTG G     | GAAGACACT     |
| CTTCTCCAAT CTGG<br>GAAGAGGTTA GACC                          | TAGACT CACT  | uGluAsp       | SerAspAsp F     | roSerVal>     |
| GAAGAGGTTA GACC<br>PheSerAsn Leuk                           | AspLeu Seroi |               |                 | 800           |
|   | 770          | 780           | 790             | * *           |
| 760   |              | * *           | * *             | no a CCTGGTC  |
| CCCTAGAGCT GTC  | CCAGCTC TCC  | ATGCTGC C     | CCACCTGGC       | ACTIGGACCAG   |
| CCCTAGAGCT GTC<br>GGGATCTCGA CAG                            | CGTCGAG AGG  | TACGACG C     | GGTGGACCG       | AspLeuVal>    |
| GGGATCTCGA CAG<br>ThrLeuGluLeu Se                           | rGlnLeu Ser  | MetLeu Pi     | COHISLEURIA     |               |
| ThriedGlubea  |              |               | 840             | 850           |
| 810   | 820          | 830           |                 | * *           |
| *   | * *          |               | GCTAAGATGA      | TACCAGGATT    |
| AGTTACAGCA TO<br>TCAATGTCGT AG                              | CAAAAGGT CA  | P V CCC P P P | CGATTCTACT      | ATGGTCCTAA    |
| TCAATGTCGT AG<br>SerTvrSer lle                              | GTTTTCCA GT  | 1eGlvPhe      | AlaLysMet       | IleProGlyPhe> |
| SerTvrSer Ile   | GlnLvsvai    | TCOT !        |                 |               |
| <b>%</b> 5  |              |               |                 |               |



# FIG. 6C

| FIG. (   |   |
|--|---|
|  | 890 900   |
| 060 870  | * * *   |
| CAGAGACCTC ACCTCTGAGG ACCAGAT                                  | * TCAAGTGCCA  |
| ACCONCTGAGG ACCAGAT  | CGT ACTGCTGAAG  |
| CAGAGACCTC ACCTCTGAGG ACCAGAT<br>GTCTCTGGAG TGGAGACTCC TGGTCTA | GCA TGACGACTIC AGTIONS  |
| GTCTCTGGAG TGGAGACTCC TGGTCTA<br>ArgAspLeu ThrSerGlu AspGlnIl  | eVal LeuLeuLys SerserArd  |
| ArgAspLeu ThrserGlu Asper                                      | 250   |
| 000  | 930 940 950   |
| 910 920  | · · · · · · · · · · · · · · · · · · ·   |
| TTGAGGTCAT CATGTTGCGC TCCAAT                                   | CACT CCTTCACCAT GGACGACATG  |
| TOTAL CATGTTGCGC TCCAAT  | CONTRACTOR |
| TTGAGGTCAT CATGTTGCGC TCCAAT<br>AACTCCAGTA GTACAACGCG AGGTTA   | CTCA GGARGETHRMET AspAspMet>  |
| AACTCCAGTA GTACAACGCG AGGTTA<br>IleGluVallle MetLeuArg SerAsn  | Glu Serrheiman  |
| IleGiuvaille   |   |
| 970  | 980   |
|  | * * CDCACCTGAC  |
| TCCTGGACCT GTGGCAACCA AGACTA                                   | ACAAG TACCGCGTCA GTGACGTCAG   |
| TCCTGGACCT GTGGCAACCA TCTGA                                    | TGTTC ATGGCGCAGT CACTGCACTO   |
| TCCTGGACCT GTGGCAACCA AGACTA<br>AGGACCTGGA CACCGTTGGT TCTGA'   | rgttc AtggcgcAgr chotologyrLys TyrArgVal SerAspValThr>  |
| SerTrpThr CysGlyAshGin Asp.                                    |   |
|  | 1030 1040 1050  |
| 1010 1020  |   |
| * * * *  | ATTGA GCCCCTCATC AAGTTCCAGG TAACT CGGGGAGTAG TTCAAGGTCC   |
| GANAGOOGGA CACAGOOTGG AGOTG                                    | CATTGA GCCCCICATO TTCAAGGTCC TTAACT CGGGGAGTAG TTCAAGGTCC LILIEGLU ProLeulle LysPheGln>   |
| CAAAGCCCT GTGTCGGACC TCGAC                                     | TAACT CGGGGACTTO  |
| GITTEGGCOT HisSerLeu GluLeu                                    | TAACT CGGGGAGTAG TITALING THE TAGE TO THE |
| Lysaladly "122"  |   |
| 1060 1070  | 1080  |
| 1060 1070  |   |
| * CANCOTGARO TTGO  | * ATGAGG AGGAGCATGT CCTGCTCATG TACTCC TCCTCGTACA GGACGAGTAC   |
| TGGGACTGAA GAAGCTCTTG AACG                                     | ATGAGG AGGAGCAIGI COLORDA AGGAGGAGTAC TTACTCC TCCTCGTACA GGACGAGTAC HisGlu GluGluHisVal LeuLeuMet>  |
| ACCCTGACTT CTTCGACTTO  | lisGlu GluGluHisVal Leubeur   |
| ValGlyLeuLys LysLeuAsii 2000                                   | 4450  |
| 4400   | 1130 1140 1150  |
| 1110 1120  | *   |
| * * * >030   | TCGTCCT GGGGTGCAGG ACGCCGCGCT AGCAGGA CCCCACGTCC TGCGGCGCGA   |
| GCCATCTGCA TCGTCTCCCC AGA                                      | ACCACGA CCCCACGTCC TGCGGCGCGA   |
| CCGTAGACGT AGCAGAGGGG TCT                                      | TCGTCCT GGGGTGCAGG TTGCGGCGCGA AGCAGGA CCCCACGTCC TGCGGCGCGCA AGCAGGA CCCCACGTCC TGCGGCGCGCA AGCAGGA CCCCACGTCC TGCGGCGCGA AGCAGGA CCCCACGTCC TGCGGCGCGCA AGCAGGA CCCCACGTCC TGCGGCGCGCGA AGCAGGA CCCCACGTCC TGCGGCGCGCA AGCAGGA CCCCACGTCC TGCGGCGCGCA AGCAGGA CCCCACGTCC TGCGGCGCGCA AGCAGGA CCCCACGTCC TGCGGCGCGCA AGCAGGA CCCCACGTCC TGCGGCGCGCGCA AGCAGGA CCCCACGTCC TGCGGCGCGCGCA AGCAGGA GCACGTCC TGCGGCGCGCACA AGCAGGA GCACGTCC TGCGGCGCGCGCACA AGCAGGA GCACGTCC TGCGGCGCGCACA AGCAGGA GCACGTCC TGCGGCGCGCACACACACACACACACACACACACACACAC  |
| AlaTleCvs IleValSerPro As                                      | <del>-</del>  |
|  | 1190 1190 1200  |
| 1160 <sup>1170</sup>   | * * *   |
| * * *  | * ACGTACATCC  |
| TO TOTAL ATTICAGGACE GC  | CTGTCCAA CACACTGCAG ACGTACATCC GACAGGTT GTGTGACGTC TGCATGTAGG   |
| GATTGAGGCC ATCCTCCTGG CG                                       | GACAGGTT GTGTGACGTC TGCATGTAGG LeuSerAsn ThrLeuGln ThrTyrlle>   |
| CTAACTCCGG TAGGICCACO  | GACAGGTT GIGIGACOTO THETYTILE> LeuSerAsn ThrLeuGln ThrTyrIle>   |
| IleGluAla IleGIMSP Mis   |   |
| 4000   | 1230 1240 1250  |
| 1210 1220  |   |
| * * *  | TO COLOR TO TOTATE CAAGATGATC   |
| CCTGCCGCCA CCCGCCCCG GC  | *  SCAGCCACC TGCTCTATGC CAAGATGATC CGTCGGTGG ACGAGATACG GTTCTACTAG LYSerHis LeuLeuTyrAla LysMetIle>   |
| CCACGGCGT GGGCGGGGC C  | CGTCGGTGG ACCULTYTALA LysMetIle>  |
| America Propropro G  | CGTCGGTGG ACGAGATACG CITYSMETILE>   |
| Argcysary  |   |
| 1260 1270  | 1280  |
| 1260 1270  |   |
| * * *  | * * AGCCTCAAT GAGGAGCACT CCAAGCAGTA TCGGAGTTA CTCCTCGTGA GGTTCGTCAT   |
| CAGAAGCTAG CCGACCIGCG  | AGCCTCAAT GAGGAGCACT  ETCGGAGTTA CTCCTCGTGA GGTTCGTCAT  SerLeuAsn GluGluHis SerLysGlnTyr>   |
| GTCTTCGATC GGCTGGACGC  | STCGGAGTTA CTCCTCGTGA GGTTGCTATYT> SerLeuAsn GluGluHis SerLysGlnTyr>  |
| GlnLysLeu AlaAspLeuArg   |   |
|  |   |

Title: "Isoforms of the Human Vitamin D Receptor" Inventor: Linda Anne Crofts

Application No.: 09/509,482 Atty. Docket No. RICE-014



1310 1320 1330 1340 1350

CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

1360 1370 1380

TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO:3) ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO:18) ValleuGluVal PheGlyAsn GlulleSer \*\*\*> (SEQ ID NO:10)

# FIG. 7A

Transcript 10 (Sequence Range: 1 to 1534) 50 20 40 MetGluTrpArg AsnLysLys> 60 70 80 90 100 AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet> 130 140 GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp> 200 160 170 180 190 GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe> 240 250 210 230 220 CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg\*\*\* (SEQ ID NO:11) 290 300 260 280 270 CCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC 330 350 310 TTTCCATGAA GGGAGCCCTT GCATTTTTCA CATCTCCTTC CTTACAATGT AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA 390 400 360 380 CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA GGTACCTTGT ACGCCGCGAG TGTCGGTGTC CTCGTCCTCC CAGAACCGCT

FIG. 7B

|                   | •          | rig. / E                 |                   |                    |
|-------------------|------------|--------------------------|-------------------|--------------------|
| 450               | 440        | 430                      | 420               | 410                |
| * *<br>CCG3CTCCCC |            | ATTCACCTGC               |                   | ACCATGAACC         |
|                   |            | TAAGTGGACG               |                   |                    |
|                   |            |                          |                   |                    |
| 500               | 490        | 480                      | 470               | 460                |
| * *               | * *        | * *                      | * *               | * *                |
|                   |            | GCCACTGCCA               |                   |                    |
| GAGTTTGCGA        | CCGGACGGCC | CGGTGACGGT               | CTGTTGGCTG        | GTAGTGGTTC         |
| 550               | 540        | 530                      | 520               | 510                |
| * *               | * *        | * *                      | * *               | * *                |
| TGAGGAAGTG        | TTCTGACAGA | AAGGAGTTCA               | CGGCATGATG        | GTGTGGACAT         |
|                   |            | TTCCTCAAGT               |                   |                    |
|                   |            |                          |                   |                    |
| 600               | 590        | 580                      | 570               | 560                |
| * *               | * *        | * *                      | * *               | * *                |
|                   |            | CCTGAAGCGG               |                   |                    |
| TCCGGAACTT        | TTCCTCCTCC | GGACTTCGCC               | CCCTCTACTA        | GTCTCCTTCG         |
| 650               | 640        | 630                      | 620               | 610                |
| * *               | * *        | * *                      | * *               | * *                |
| ATCATTGCCA        | GCAGCAGCGC | TGTCTGAGGA               | CGGCCCAAGC        | GGACAGTCTG         |
|                   |            | ACAGACTCCT               |                   |                    |
|                   |            |                          |                   |                    |
| 700               | 690        | 680                      | 670               | 660                |
| * *               | * *        | * *                      | * *               | * *                |
|                   |            | AAGACCTACG               |                   |                    |
| GAGGCTGAAG        | TGGGGTGGAT | TTCTGGATGC               | GCGGGTGGTA        | ATGACGACCT         |
| 750               | 740        | 730                      | 720               | 710                |
| * *               | * *        | * *                      | * *               | * *                |
| GGAGCCATCC        | GATGGTGGAG | TCGTGTGAAT               | GGCCTCCAGT        | TGCCAGTTCC         |
| CCTCGGTAGG        | CTACCACCTC | AGCACACTTA               | CCGGAGGTCA        | ACGGTCAAGG         |
|                   |            |                          |                   |                    |
| 800               | 790        | 780                      | 770               | 760                |
| * *               | * *        | * *                      | * *               | * *                |
|                   |            | ACACTCCCAG<br>TGTGAGGGTC |                   |                    |
| CIGNGGAGGA        | GAAGAGACCC | IGIGNGGGIC               | 11GAGGICIG        | ANGGICCGGG         |
| 850               | 840        | 830                      | 820               | 810                |
| * *               | * *        | * *                      | * *               | * *                |
| GGACTCGTCC        | CAGACATGAT | ATCACCTCTT               | AGATCACTGT        | CCTCCTGCTC         |
| CCTGAGCAGG        | GTCTGTACTA | TAGTGGAGAA               | TCTAGTGACA        | GGAGGACGAG         |
|                   |            |                          |                   |                    |
| 900               | 890        | 880                      | 870               | 860                |
|                   | ~ ×        | GAGTGAAGAA               | * *<br>3mcmcc3mcm | እ <i>ርር</i> መውርመምር |
|                   |            | CTCACTTCTT               |                   |                    |
| 2 GGGAAGACA       | CIMMOTOTAC | CICACIICIT               |                   |                    |
| 950               | 940        | 930                      | 920               | 910                |
| * *               | * *        | * *                      | * *               | * *                |
|                   |            | TCTCCATGCT               |                   |                    |
| CGACTGGACC        | CGGGGTGGAC | AGAGGTACGA               | GACAGGGTCG        | CTGGGATCTC         |
|                   |            |                          |                   |                    |

# FIG. 7C

|                                 | FIG                                      | . 7C                       |                         |                  |                      |
|---------------------------------|--|----------------------------|-------------------------|------------------|----------------------|
|                                 | , , ,                                    |                            | 990                     | 1                | 000                  |
| 960                             | 970                                      | 980<br>• *                 | * *                     | *                | *                    |
|                                 | * *                                      | <sub>TTGGCT</sub> TTG      | CTAAGAT G               | ATACCA           | ⊾GGA                 |
| TCAGTTACAG CATO                 | CAAAAG GICA<br>GTTTTC CAGT               | AACCGA AAC                 |                         |                  |                      |
|                                 | 1020                                     | 1030                       | 1040                    |                  | 1050<br>*            |
| 1010                            | * *                                      | * *                        | * *                     | AGTCAA           | GTGC                 |
| TTCAGAGACC TCA                  | CCTCTGA GGA<br>GGAGACT CCT               | CCAGATC GTA<br>GGTCTAG CA  |                         | TCAGTT           | CACG                 |
|                                 | 1070                                     | 1080                       | 1090                    | *                | *                    |
| 1060                            | * *                                      | * *                        | * * *                   | ATGGA(           | CGACA                |
| * * CATTGAGGTC AT GTAACTCCAG TA | CATGTTGC GCT<br>GTACAACG CG              | CCAATGA GT<br>AGGTTACT CA  |                         | TACCT            |                      |
|                                 | 1120                                     | 1130                       | 1140                    |                  | 1150                 |
| 1110                            | 1120                                     |                            | * *                     |                  | 2ACGTG               |
| TGTCCTGGAC CT<br>ACAGGACCTG G   | rgtggcaac ca<br>acaccgttg gi             | AGACTACA A<br>TCTGATGT T   | GTACCGCGT<br>CATGGCGCA  | GTCAC            |                      |
| ACAGONOTE                       |  | 1180                       | 1190                    | )                | 1200                 |
| 1160                            | 1170                                     |                            | *                       | k                | * -                  |
| ACCAAAGCCG C                    | ACACAGCCT G                              | GAGCTGATT (<br>CTCGACTAA ( | GAGCCCCTC<br>CTCGGGGAG  | A TCAA<br>T AGTT |                      |
| 19911100                        |  | 1230                       | 124                     | <b>.</b> 0       | 1250                 |
| 1210                            | 1220                                     |                            | *                       | *                | * ~ ~                |
| # * GGTGGGACTG                  | AAGAAGCTGA I<br>TTCTTCGACT '             | ACTTGCATGA<br>IGAACGTACT   | GGAGGAGC!<br>CCTCCTCG!  | TA CAG           |                      |
| CCACCCIO                        |  | 1280                       | 12                      | 90               | 1300                 |
| 1260                            | 1270                                     |                            | *                       | *                | * *                  |
| TGGCCATCTG                      | * * CATCGTCTCC GTAGCAGAGG                | CCAGATCGTC<br>GGTCTAGCAG   | CTGGGGTG<br>GACCCCAC    | CA GGP<br>GT CCT | LGCGGCGC<br>FCGCCGCG |
| ACCGGTAGAC                      | GIAGONG                                  |                            | . 13                    | 340              | 1350                 |
| 1310                            | 1320                                     | 1330                       | , -                     | *                | * *                  |
|                                 | . *                                      | •                          |                         | TGC AG           | ACGTACAT             |
| CTGATTGAGC                      | * * CCATCCAGGA GGTAGGTCCT                | GGCGGACAG                  | G TTGTGTG               | ACG TO           |                      |
| Grio                            |  |                            |                         | 390              | 1400<br>* *          |
| 136                             | 0 1370                                   |                            |                         | *                | * "                  |
| CCGCTGCCG                       | * CACCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC | C CGGGCAGC(<br>G GCCCGTCG( | CA CCTGCTO<br>GT GGACGA | CTAT G           |                      |
| GGCGRCGG                        |  |                            | 30                      | 1440             | 7.204                |
| 143                             | 10 142                                   | . •                        |                         | *                | * *                  |
| *<br>TCCAGAAG<br>AGGTCTTC       | * * CT AGCCGACCT                         | ••                         |                         | AGCA (           |                      |
|                                 |  |                            | 400                     | 1490             |                      |
| 14                              | 160 14                                   |                            |                         | *                | * *<br>->>>CCCCCT    |
| TACCGCTY<br>ATGGCGA             | GC TCTCCTTC                              |                            |                         | GAAGC<br>.CTTCG  | ATTGCGGGGA           |



# FIG. 7D

1520 1510

1530

TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4)

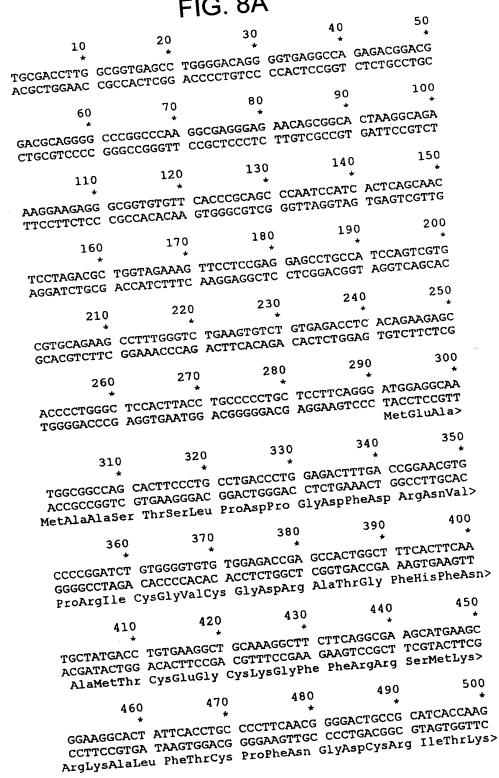
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)



Title: "Isoforms of the Human Vitamin D Receptor" Inventor: Linda Anne Crofts

Application No.: 09/509,482 Atty. Docket No. RICE-014

#### FIG. 8A





| n san s  |   |           |                   |                 |               |
|--|---|-----------|-------------------|-----------------|---------------|
| FIG. 8B  |   |           |                   |                 |               |
|  |   | 530       | 540               | 550             | )<br>*        |
| 510  | 520   | *         | *                 | rcrccaca'       | T             |
| 510  * GACAACCGAC GCCAC                                  | mccca GGCCT(                                      | CCGG CTC  | AAACGCT G         | ACACCTGT        | A             |
| GACAACCGAC GCCAC   | ACGGT CCGGA                                       | CGGCC GAG | T∩eVia CA         | sValAspI        | le>           |
| GACAACCGAC GCCAC<br>CTGTTGGCTG CGGTC<br>AspAsnArg ArgHi: | sCysGln AlaC                                      | ysArg Leu | ПАрта             | 60              | <b>10</b>     |
|  |   | 300       |                   |                 |               |
| 560  | 570<br>*  | <b>*</b>  | *                 | AGAGGAA         | GC            |
| CGGCATGATG AAGG  | AGTTCA TTCT                                       | ACAGA TGA | TCCTTCAC          | GTCTCCTT        | CG            |
| CGGCATGATG AACC  | TCAAGT AAGA                                       | CTGTCT AC | luGluVal          | GlnArgLy        | s>            |
| CGGCATGATG AAGG<br>GCCGTACTAC TTCC<br>GlyMetMet LysC     | SluPhe IleLe                                      | Ullivab . |                   | 6               | 550           |
|  |   | 630       |                   |                 | •             |
| 610  * GGGAGATGAT CCT                                    |   | *         | -ссстт <b>GAA</b> | GGACAGT         | CTG           |
| GGGAGATGAT CCT<br>CCCTCTACTA GGA                         | GAAGCGG AAGC                                      | AGGAGG AG | CCGGAACTT         | CCTGTCA         | GAC<br>Lau>   |
| CCCTCTACTA GGA   | CTTCGCC TTC                                       | SluGlu Gl | uAlaLeuLy         | s Aspser        | Dear          |
| GGGAGATGAT CCT<br>CCCTCTACTA GGA<br>ArgGluMetIle Le      | euLysArg Lys                                      |           | 690               |                 | 700           |
|  |   |           |                   |                 |               |
| CGGCCCAAGC TG  | *   | CCNCCGC P | ATCATTGCC#        | TACTGC          | rgga<br>Nacat |
| CGGCCCAAGC TG<br>GCCGGGTTCG AC                           | TCTGAGGA GCA                                      | CGTCGCG   | ragtaacgg"        | ATGACGA<br>LeuL | euAsp>        |
| GCCGGGTTCG AC  | AGACTUCT CG                                       | lnGlnArg  | IleIleAla         | TIEBCGE         |               |
| CGGCCCAAGC TG<br>GCCGGGTTCG AC<br>ArgProLys Let          | 12610100-   | _         | 74                | 0               | 750           |
|  |   | 130       |                   |                 |               |
| 710 * CGCCCACCAT A GCGGGTGGTA T                          | - argamaca AC                                     | CCCACCTA  | CTCCGACTT         | C ACGGT         | CAAGG         |
| CGCCCACCAT A   | AGACCIACO TO                                      | GGGTGGAT  | GAGGCTGA          | ne CysGli       | nPhe>         |
| GCGGGTGGTA I   | AGACCTACG AC<br>TCTGGATGC TO<br>ysThrTyr Asi      | ProThrTy  | 1 20231           |                 | 800           |
|  |   | 100       |                   |                 | *-            |
| 760  |   | *         | TANCCCCAT         | CC TTCC         | /GGCCC        |
|  | TCGTGTGAAT G                                      | ATGGTGGAG | CCTCGGTA          | AGG AAGG        | CCGGG         |
| GGCCTCCAGT<br>CCGGAGGTCA<br>ArgProProVal                 | TCGTGTGAAT G<br>AGCACACTTA C<br>ArgValAsn I       | TACCACCIC | GlySerHis         | Pro Ser         | Argrio        |
| ArgProProVal   | ArgValAsn F                                       | (Spor) 1  |                   | 040             | 850           |
| 210  | 820   | 63        | <u>.</u>          | *               | ••            |
| 810  |   |           | G GACTCCT         | CCT CCTC        | CTGCTC        |
| AACTCCAGAC   | ACACTCCCAG<br>TGTGAGGGTC                          | CANGAGACO | C CTGAGGA         | GGA GGAG        | crCvsSer>     |
| TTGAGGTCTG   | ACACTCCCAG<br>TGTGAGGGTC<br>HisThrProSer          | PheSerGl  | Ly AspSerS        | ser sers        | 210]-         |
| AsnSerArg  | HISTRIFIC   |           | _                 | 890             | 900           |
|  | 020   | 9.        | 80                |                 | •             |
| ,  | *   | CAGACATG  | AT GGACTC         | GTCC AGC        | AAGAGGT       |
| AGATCACTG'   | * TATCACCTCTT ATAGTGGAGAA                         | GTCTGTAC  | TA CCTGAG         | CAGG ICC        | PheSer>       |
| TCTAGTGAC  | T ATCACCTCTT<br>A TAGTGGAGAA<br>s IleThrSer       | SerAspMet | Met Aspse         | IDEL -          | 25.0          |
| AsphisCy   | 5 1100  |           | 930               | 940             | 950<br>*      |
| 91   | 10 92   | •         | *                 | *<br>           | CCCTAGAG      |
| _  | CT GAGTGAAGA                                      | A GATTCAG | ATG ACCCT         | AGACA CI        | GGGATCTC      |
| ATCTGGAT   | *<br>CT GAGTGAAGA<br>GA CTCACTTCT<br>Leu SerGluGl | T CTAAGTC | TAC TEGGA         | SerVal T        | hrLeuGlu>     |
| TAGACCIA   | Leu SerGluGl                                      | u AspSerA | rah vaher.        |                 | 1000          |
|  |   | - ^       | 900               |                 |               |
| ġ  | 960   |           | *<br>mc_ccmc      |                 | CAGTTACAG     |
| amacca   | AGC TCTCCATG                                      | CT GCCCCA | CCTG GCTG         | TGGACC A        | GTCAATGTC     |
| CTGTCCC<br>CACAGGG                                       | *<br>AGC TCTCCATG<br>TCG AGAGGTAC<br>ln LeuSerMet | GA CGGGGT | sLeu AlaA         | spLeu Va        | ISerryLacio   |
| LeuSerG  | ln LeuSerMet                                      | Ter Lrour |                   |                 |               |
|  |   |           |                   |                 |               |



Title: "Isoforms of the Human Vitamin D Receptor"

Inventor: Linda Anne Crofts Application No.: 09/509,482 Atty. Docket No. RICE-014

FIG. 8C 1040 1030 CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG IleGlnLys VallleGly PheAlaLysMet IleProGly PheArgAsp> 1080 TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal> 1130 ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr> 1180 CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla> 1230 GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu> 1280 AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys> 1330 CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu> 1400 1380 CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC 1370 GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG AlaileGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg> 1430 CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu> 1480 AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>

OT 2 2 2002

Title: "Isoforms of the Human Vitamin D Receptor"

Inventor: Linda Anne Crofts Application No.: 09/509,482 Atty. Docket No. RICE-014

#### FIG. 8D

1510

1520

1530

1540

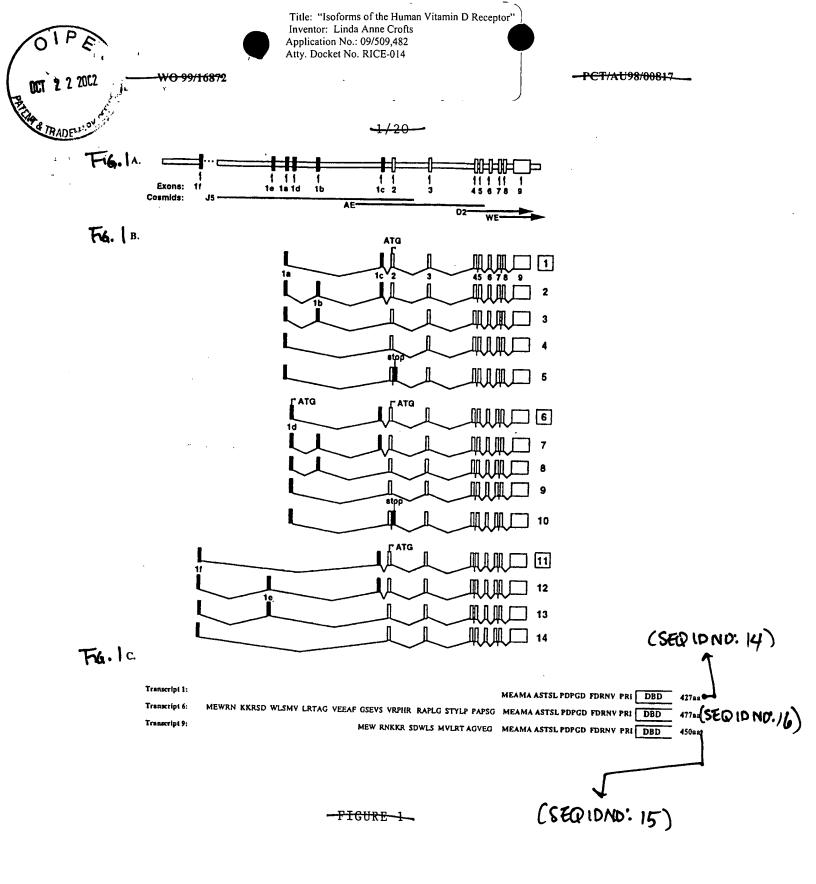
1550

TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

1560

1570

GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:7) CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:20) ValPheGly AsnGluIleSer \*\*\*> (SEQ ID NO:12)



Inventor: Linda Anne Crofts Application No.: 09/509,482 Atty. Docket No. RICE-014

<del>WO 99/16872 </del>

PCT/AU98/00817

4/20-

- 5'...tgtttttagAGGCAGCATGAAACAGTGGGATGTGCAGAGAGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGTAGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAACGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAAAGATCAAgtaagatatt...3' (SEQIDNO: (,))

FIG. 4

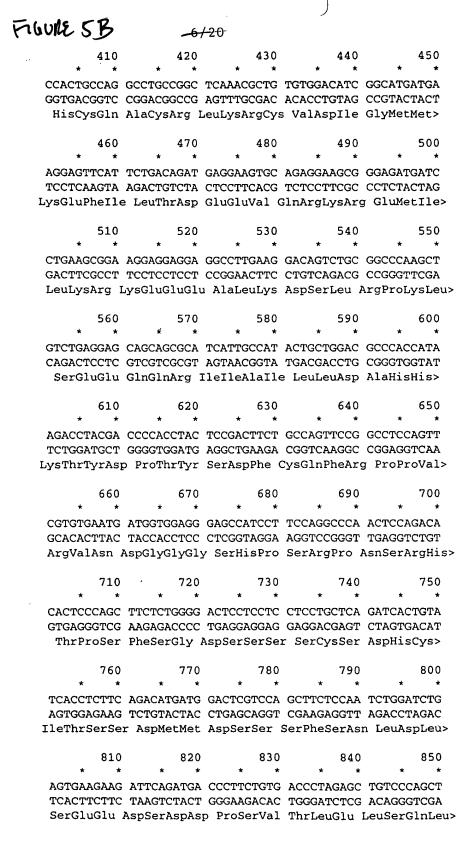
PCT/AU98/00817

|               | <del>-5/</del>  | 20-                                    |   |   |  |
|---------------|---|--|---|---|--|
| G. 5A         | TRANSCRIP   | г 6                                    |   |   |  |
| (Sequence Rai | nge: 1 to 1463)   |  |   |   | 50   |
|               | 10  | 20                                     | 30  | 40  | * *  |
|               | * * * GTTTCCTTCT TCTGT CAAAGGAAGA AGACA                   | *<br>GCCCC GCC<br>AGCCCC GCC           |   | AGTGGAG GAA<br>TCACCTC CT<br>JuTrpArg A   | \TAAGAAA<br>FATTCTTT<br>snLysLys>          |
|               |   |  | 80  | 90  | 100  |
|               | 60  | 70                                     |   | * *                                       | * *  |
|               | * * AGGAGCGATT GGCT<br>TCCTCGCTAA CCGA<br>ArgSerAsp TrpLe | *<br>GTCGAT GG<br>CAGCTA CC            | TGCTCAGA AC<br>ACGAGTCT TG<br>ValleuArg Th  | TGCTGGAG TG<br>ACGACCTC AC<br>rAlaGly Val | IGIUGIUALA                                 |
|               | 1123  |  | 130   | 140                                       |  |
|               | 110   | 120                                    |   | * *                                       | •  |
|               | CTTTGGGTCT GAA<br>GAAACCCAGA CTT<br>PheGlySer Glu         | GTGTCTG T<br>CACAGAC A<br>Valser Va    | GAGACCTCA CA<br>CTCTGGAGT G<br>AlArgProHis  | AGAAGAGCA C<br>TCTTCTCGT G<br>ArgArgAla F | )[Olegor]                                  |
|               |   | 170                                    | 180   | 190                                       | 200  |
|               | CCACTTACCT GCC<br>GGTGAATGGA CG<br>SerThrTyrLeu P         | CCCCTGCT<br>GGGGACGA<br>roProAla       | CCTTCAGGGA T<br>GGAAGTCCCT A<br>ProSerGly M | rGGAGGCAAT<br>ACCTCCGTTA<br>etGluAlaMet   | Alaniaber                                  |
| •             | DCI 111   |  | . 230                                       | 240                                       | 250  |
|               | 210   | 220                                    |   | * *                                       | •  |
|               | ACTTCCCTGC CT<br>TGAAGGGACG GA<br>ThrSerLeu Pro           | rGACCCTGG<br>ACTGGGACC<br>oAspProG1    | y AspPheAsp                                 | CGGAACGTGC<br>GCCTTGCACG<br>ArgAsnVal     | 300  |
|               | 260   | 270                                    | 280   |   | * *  |
|               | TGGGGTGTGT G ACCCCACACA G                                 | *<br>GAGACCGA<br>CTCTGGCT<br>GlyAspArg | CCACTGGCTT GGTGACCGAA AlaThrGlyPt           | TCACTTCAAT<br>AGTGAAGTTA<br>Ne HisPheAs   | n Alametini                                |
|               | GIJ van-1   |  | 22  |   | 0 350                                      |
|               | 310   | 32<br>*                                | * *   | * *                                       | * * * *<br>G GAAGGCACTA                    |
|               | GTGAAGGCTG<br>CACTTCCGAC<br>CysGluGlyCys                  | CAAAGGCTT<br>GTTTCCGA<br>LysGlyP       | C TTCAGGCGA<br>AG AAGTCCGCT<br>he PheArgArg | T CGTACTTCC                               | CG GAAGGCACTA GC CTTCCGTGAT Arg LysAlaLeu: |
|               |   |  |   | 30 3                                      | 90 400                                     |
|               | 360<br>* *  | *                                      | * *   | * *<br>GC ATCACCAA                        | ,GG ACAACCGACG<br>,GG TGTTGGCTGC           |
|               | TTCACCTGCC<br>AAGTGGACGG<br>PheThrCys                     | GGAAGTTC<br>GGAAGTTC<br>ProPheAsi      | GCC CCTGACGG                                | CG TAGTGGTT<br>rg lleThrL)                | CC TGTTGGCTGC AspAsnArgAr                  |

:G PheThrCys ProPheAsnGly AspCysArg | IleThrLys AspAsnArgArg>

WO 99/16872

PCT/AU98/00817



-PCT/AU98/00817-

F19.7A

| 74. 74       | TRANSCRIP  | 10  |  |   |                                   |
|--------------|--|---|--|---|-----------------------------------|
| a Ds         | ange: 1 to 1534)   |   |  |   | 50                                |
| (Sequence Re | ange   |   | 30   | 40  | 5U<br>* *                         |
|              | 10   | 20  |  | * *   | *                                 |
|              | * * TOTTCCTTCT TCTGCAAAGGAAGA AGAC                           | * *<br>TCGGGG CGC<br>AGCCCC GCC               | *<br>CTTGGCA TG:<br>GAACCGT AC<br>Met        | GAGTGGAG GA<br>CTCACCTC CT<br>GluTrpArg A   |                                   |
|              |  |   |  | 90  | 100                               |
|              | <b></b>  | 70  | 80   |   | * *                               |
| •            | 60   | *   | * *  | *   | GAGGGGAT                          |
|              | AGGAGCGATT GGCTCCTCGCTAA CCGArgSerAsp TrpL                   | rGTCGAT GG<br>ACAGCTA CC<br>euSerMet \        | TGCTCAGA A<br>ACGAGTCT T<br>ValleuArg T      | CTGCTGGAG TO<br>GACGACCTC A<br>ChrAlaGly Va | CCTCCCCTA 1GluGlyMet>             |
|              | Argsernop  |   | 130  | 140   | 150                               |
|              | 110  | 120   |  | * *   | *                                 |
|              |  | * *   | * ~~   | TCACCCTGGA                                  | BACTTTGACC                        |
|              | 110  * *  GGAGGCAATG GCC CCTCCGTTAC CGC GluAlaMet Al         | GCCAGCA C<br>CCGGTCGT (<br>aAlaSer Th         | TTCCCTGCC<br>AAGGGACGG<br>rSerLeuPro         | ACTGGGACCT ( AspProGly                      | TGAAACTGG<br>AspPheAsp>           |
|              | GIONIA   |   | 180  | 190   | 200                               |
|              | 160  | 170   |  | * *   | * "                               |
|              | 160<br>* *<br>GGAACGTGCC CC<br>CCTTGCACGG GC<br>ArgAsnValPro | * CGGATCTGT CCTAGACA ArgileCys                | GGGGTGTGTG<br>CCCCACACAC<br>GlyValCys<br>230 | GlyAsparava                                 | 250                               |
|              | 210  | 220   |  |   | ж                                 |
|              | · · · · · · · · · · · · · · · · · · ·                        | * *<br>CTATGACCTG<br>GATACTGGAC<br>LaMetThrC) | TGAAGGCTG<br>ACTTCCGAC<br>S GluGlyCy         | C AAAGGCTTCT<br>G TTTCCGAAGA<br>S LysGlyPhe | TCAGGTGAGC A AGTCCACTCG PheArg*** |
| •            | Hisphens   |   |  | 29  | 0 300                             |
|              | 260  | 27  | 0 28   |   | * * *                             |
|              |  | * GGCTCTCCC CCGAGAGGG                         | * *<br>C AGTGGAAA<br>G TCACCTTT              | GG GAGGGAGAA<br>CC CTCCCTCTT                | AG AAGCAAGGTG TTCGTTCCAC 40 350   |
|              | GGGGAGGG1  | 000   |  |   | 40 350                            |
|              | 310  | 33  |  | 30  | _ * *                             |
|              | TTTCCATGA  | * GGGAGCCC                                    | * *<br>TT GCATTTT<br>AA CGTAAAA              | -   | TC CTTACAATGT AG GAATGTTACA 400   |
|              | AAAGGTACT  |   |  |   | 400                               |
|              |  | -   | 170  | 380   | * *                               |
|              | 36   |   | * *  | * *   | - CTCTTGGCGA                      |
|              | *<br>CCATGGAAC<br>GGTACCTTG                                  | * TGCGGCGGCGC                                 |  |   | AGG GTCTTGGCGA<br>TCC CAGAACCGCT  |



Title: "Isoforms of the Human Vitamin D Receptor" Inventor: Linda Anne Crofts

Application No.: 09/509,482
Atty. Docket No. RICE-014

PCT/AU98/00817-

FIG. 7B

| 410          | 420        | 430                | 440                      | 450        |
|--------------|------------|--------------------|--------------------------|------------|
| * *          | * *        | * *.               | * *                      | * *        |
|              |            |                    | CCCTTCAACG               |            |
| TCGTACTTCG   | CCTTCCGTGA | TAAGTGGACG         | GGGAAGTTGC               | CCCTGACGGC |
| 460          | 470        | 480                | 490                      | 500        |
| * *          | * *        | * *                | * *                      | * *        |
| CATCACCAAG   | GACAACCGAC | GCCACTGCCA         | GGCCTGCCGG               | CTCAAACGCT |
|              |            |                    | CCGGACGGCC               |            |
|              |            |                    |                          |            |
| 510          | 520        | 530                | 540                      | 550        |
| * *          | * *        | * *                | * *                      | * , *      |
| GTGTGGACAT   | CGGCATGATG | ${\tt AAGGAGTTCA}$ | TTCTGACAGA               | TGAGGAAGTG |
| CACACCTGTA   | GCCGTACTAC | TTCCTCAAGT         | AAGACTGTCT               | ACTCCTTCAC |
|              |            |                    |                          |            |
| 560          | 570        | 580                | 590                      | 600        |
| * *          | * *        | * *                | * *                      | * *        |
|              |            |                    | AAGGAGGAGG               |            |
| GTCTCCTTCG   | CCCTCTACTA | GGACTTCGCC         | TTCCTCCTCC               | TCCGGAACTT |
| 610          | 620        | 630                | 640                      | 650        |
| * *          | * *        | * *                | * *                      | * *        |
| GGACAGTCTG   | CGGCCCAAGC | ТСТСТСАССА         | GCAGCAGCGC               | АТСАТТСССА |
|              |            |                    | CGTCGTCGCG               |            |
|              |            |                    |                          |            |
| 660          | 670        | 680                | 690                      | 700        |
| * *          | * *        | * *                | * *                      | * *        |
|              |            |                    | ACCCCACCTA               |            |
| ATGACGACCT   | GCGGGTGGTA | TTCTGGATGC         | TGGGGTGGAT               | GAGGCTGAAG |
| <b>5</b> 4.0 |            |                    | 540                      | 550        |
| 710          | 720        | 730                | 740                      | 750        |
| mcccycmmcc   |            |                    | GATGGTGGAG               | GCACCCATCC |
|              |            |                    | CTACCACCTC               |            |
| ACGGICAAGG   | CCGGAGGICA | AGCACACTTA         | CIACCACCIC               | CCICGGIAGG |
| 760          | 770        | 780                | 790                      | 800        |
| * *          | * *        | * *                | * *                      | * *        |
| TTCCAGGCCC   | AACTCCAGAC | ACACTCCCAG         | CTTCTCTGGG               | GACTCCTCCT |
| AAGGTCCGGG   | TTGAGGTCTG | TGTGAGGGTC         | GAAGAGACCC               | CTGAGGAGGA |
|              |            |                    |                          |            |
| 810          | 820        | 830                | 840                      | 850        |
| * *          | * *        |                    |                          | * *        |
|              |            |                    |                          | GGACTCGTCC |
| GGAGGACGAG   | TCTAGTGACA | TAGTGGAGAA         | GTCTGTACTA               | CCTGAGCAGG |
| 860          | 870        | 880                | 890                      | 900        |
| * *          |            | * * *              | * *                      | * * *      |
|              |            |                    | GATTCAGATG               |            |
|              |            |                    | CTAAGTCTAC               |            |
|              |            |                    |                          |            |
| 910          | 920        | 930                | 940                      | 950        |
| * *          | * *        | * *                |                          |            |
| 0100001010   |            |                    |                          |            |
|              |            | TCTCCATGCT         | GCCCCACCTG<br>CGGGGTGGAC |            |

-PCT/AU98/00817

| <b>r</b>   | -11                                       | 7C                              |   |                               |   |   |   |
|--|---|---------------------------------|---|-------------------------------|---|---|---|
| F  | -19:                                      | 20                              |   |                               |   |   |   |
|  |   | 98                              | 10                                      | 990                           |   | *<br>1000                                     |   |
| 960  | 970                                       | *                               | * 1                                     | * *                           | ማመንሮር<br>"                              | agga  |   |
| 960<br>* *<br>TCAGTTACAG CATC<br>AGTCAATGTC GTAG | * * *                                     | CATTGG                          | CT TTGC                                 | TAAGAT                        | CTATGG                                  | TCCT  |   |
| TCAGTTACAG CATO                                  | CAAAAG GI                                 | GTAACC                          | GA AACG                                 | ATTCTA                        | CIMIC                                   |   |   |
| AGTCAATGTC GTA                                   | GG I I I I C O.                           |                                 |   | 1040                          | )                                       | 1050  |   |
|  |   | 1.1                             | 130                                     |                               | . *                                     | •   |   |
| 1010   |   | *                               | *<br>አመሮ ርሞል(                           | TGCTG                         | A AGTCA                                 | AGTGC   |   |
| 1010  * *  TTCAGAGACC TCA                        | ACCTCTGA G                                | GACCAG                          | TAG CAT                                 | GACGAC                        | T TCAGT                                 | TCACG   |   |
| * * TTCAGAGACC TCA AAGTCTCTGG AG                 | TGGAGACT C                                | CTGGTC                          | INO -                                   |                               | _                                       | 1100  |   |
|  |   | 1                               | UBU                                     |                               |   | k "   |   |
| 1060   | 1070                                      | *                               | *                                       | *                             | T ATGG                                  | ACGACA  |   |
| 1060<br>* *<br>CATTGAGGTC AT<br>GTAACTCCAG TA    | *<br>************************************ | GCTCCA                          | ATGA GTO                                | CTTCA                         | GG TACC                                 | $_{ m TGCTGT}$                                |   |
| CATTGAGGTC AT                                    | CMACAACG                                  | CGAGGT'                         | TACT CAG                                | AMG                           | 00                                      |   |   |
| GTAACTCCAG TA                                    | AGINGIA                                   |                                 |   | 11                            | 40                                      | 1150  |   |
|  |   |                                 | 1130                                    |                               |   | *   |   |
| * *  | * *                                       | ~> > C > (                      | TACA AC                                 | TACCG                         | CGT CAG                                 | rGACGIC<br>a crgCAC                           |   |
| 1110  * * TGTCCTGGAC C                           | TGTGGCAAC                                 | CAAGA                           | GATGT TO                                | CATGGC                        | GCA GTC                                 | ACTOOL  |   |
| TGTCCTGGAC C<br>ACAGGACCTG C                     | GACACCGTTG                                | GIIO-                           |   |                               | 190                                     | 1200  |   |
|  |   |                                 | 1180                                    |                               |   | * "   |   |
| 1160   |   | . *                             | mm C                                    | 'AGCCCC                       | CTCA TC                                 | AAGTTCCA                                      |   |
| 1160<br>* *<br>ACCAAAGCCG<br>TGGTTTCGGC          | GACACAGCC                                 | T GGAG                          | TGATT C                                 | TCGGG                         | GAGT AG                                 | TTCAAGGT                                      |   |
| ACCAAAGCCG                                       | CTGTGTCGG                                 | A CCTC                          | JACTAN S                                |                               |   | 1250  |   |
|  |   |                                 | 1230                                    |                               |   | *   |   |
| 1210   | 122                                       | k.                              | * *                                     | *                             | 00                                      | CCTGCTCA                                      |   |
| 1210<br>* *<br>GGTGGGACTG<br>CCACCCTGAC          | * * * * * * * * * * * * * * * * * * *     | GA ACTI                         | GCATGA                                  | GGAGG!                        | rCGTA C                                 | AGGACGAGT                                     |   |
| GGTGGGACTG                                       | HTCTTCGA                                  | CT TGA                          | ACGTACT                                 | CCICC                         | 100-                                    | 1200  |   |
| CCACCCTGAC                                       |   |                                 | 1280                                    |                               | 1290                                    | 1300  |   |
| 126  | 0 12                                      | 270                             | * *                                     | *                             | *                                       | an caccaca                                    |   |
| *  | * *                                       | *<br>                           | GATCGTC                                 | CTGGC                         | GTGCA (                                 | GGACGCCGCG<br>CCTGCGGCGC                      |   |
| $_{\mathrm{TGGCCATCT}}$                          | G CATCGTC                                 | AGG GG                          | CTAGCAG                                 | GACC                          | CCACGI                                  | CCTGCGGCGC                                    |   |
| ACCGGTAGA  | AC GTAGCAG                                | ACC -                           |   |                               | 1340                                    | 1350  |   |
|  |   |                                 | 133                                     | U                             |   | * "   |   |
| 13.  | TO  |                                 | *                                       | C AACA                        | CACTGC                                  | AGACGTACAT                                    |   |
| aman mmGA  | GG CCATCC                                 | AGGA CC                         | CCCACAC                                 | G TTG                         | rgtgacg                                 | AGACGTACAT<br>TCTGCATGTA                      |   |
| CACTAACT   | CC GGTAGG                                 | TCCT G                          | ,00::0                                  |                               | 1390                                    | 1400  |   |
|  |   |                                 | 1.34                                    | 00                            |   | *   |   |
| 13   | 360                                       |                                 | *                                       | *                             |   | ADPAGA AGARA                                  |   |
| *  | *<br>************************************ | GCCCC C                         | GGGCAGC                                 | CA CC                         | CGAGAT                                  | A CGGTTCTACT                                  |   |
| CCGCTGC  | 1 (30 0220 -                              |                                 | ᠂ᡣᢗᢗᢗᢗ                                  | JUN 1001                      |   |   |   |
|  | CCG GTGGG                                 | CGGGG                           | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, |                               |   | 1/50  |   |
| GGCGACC  | GCG GTGGG                                 |                                 |   |                               | 144                                     | 0 1450  |   |
|  | 1410                                      | 1420                            | *                                       | 430<br>*                      | 144                                     | 0 1450<br>* * *                               |   |
|  | 1410                                      | 1420                            | *                                       | 430<br>*                      | 144                                     | 0 1450<br>* * *                               |   |
|  | 1410                                      | 1420                            | *                                       | 430<br>*                      | 144                                     | 0 1450<br>* * *                               |   |
|  | 1410                                      | 1420                            | t<br>CGCAGCC<br>GCGTCGG                 | 430<br>*<br>TCA AT            | 144<br>*<br>CGAGGAGC<br>ACTCCTCC        | * * * A CTCCAAGCAG ET GAGGTTCGTC              | 1 |
| *<br>TCCAGA<br>AGGTCT                            | AGCT AGCC                                 | 1420<br>* *<br>GACCTG<br>CTGGAC | * CGCAGCC GCGTCGG                       | 430<br>*<br>TCA AT<br>GAGT TA | 144<br>*<br>CGAGGAGC<br>ACTCCTCC        | 0 1450  * * CTCCAAGCAG GT GAGGTTCGTC  90 1500 | • |
| TCCAGA<br>AGGTCT                                 | AGCT AGCC<br>TCGA TCGG                    | 1420  * * * GACCTG CTGGAC 1470  | CGCAGCC<br>GCGTCGG                      | 430<br>*<br>TCA AT<br>GAGT TA | 144<br>*<br>CGAGGAGC<br>ACTCCTCC<br>14  | A CTCCAAGCAG GT GAGGTTCGTC  90 1500           | r |
| TCCAGA<br>AGGTCT                                 | 1410 AGCT AGCC TCGA TCGG                  | 1420  * * * GACCTG CTGGAC 1470  | CGCAGCC<br>GCGTCGG                      | 430<br>*<br>TCA AT<br>GAGT TA | 144<br>**<br>CGAGGAGC<br>ACTCCTCC<br>14 | A CTCCAAGCAG GT GAGGTTCGTC  90 1500           | r |
| TCCAGA<br>AGGTCT                                 | 1410 AGCT AGCC TCGA TCGG                  | 1420  * * * GACCTG CTGGAC 1470  | CGCAGCC<br>GCGTCGG                      | 430<br>*<br>TCA AT<br>GAGT TA | 144<br>**<br>CGAGGAGC<br>ACTCCTCC<br>14 | * * * A CTCCAAGCAG ET GAGGTTCGTC              | r |

<del>-WO 99/16872-</del>

Title: "Isoforms of the Human Vitamin D Recept

Inventor: Linda Anne Crofts Application No.: 09/509,482 Atty. Docket No. RICE-014

PCT/AU98/00817\_

1510

1520

1530

TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4)
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)

Title: "Isoforms of the Human Vitamin D Inventor: Linda Anne Crofts Application No.: 09/509,482

| - Licotion   | nda Anne Croft<br>No.: 09/509,482<br>No. RICE-014 |   |  | <del>−PCT/AU9</del>                       | 8/00817                   |
|--|---|---|--|---|---------------------------|
| 2_   |   |   |  |   |                           |
|  | -17/2   | 9—  |  |   |                           |
| 7. 0 /7<br>FIGURE 8 TR                                   | ANSCRIPT  |   | 40                                     | 50  |                           |
|  | 20  | 30  |  | *   |                           |
| TGCGACCTTG GCGGTC  | *<br>BAGCC TGGG<br>CTCGG ACCC                     | GACAGG GG                                   | TGAGGCCA (                             |   |                           |
| ACGCTGGAAC CGCCAC  |   | 80  | 90                                     | 10  | )<br>*                    |
| 60   | 70<br>*   |   | *                                      | CTAAGGCAG                                 | A                         |
| 60<br>*<br>GACGCAGGGG CCCGG<br>CTGCGTCCCC GGGCC          | CCCAA GGC<br>CGGTT CCG                            | GAGGGAG A<br>CTCCCTC T                      |  | GATTCCGTC                                 | T<br>50                   |
| 010-   | 100   | 130   | 140                                    |   | *                         |
| 110<br>*<br>AAGGAAGAGG GCGG                              |   | *<br>CCCGCAGC (<br>GGGCGTCG (               | CCAATCCATC<br>GGTTAGGTAG               | ACTCAGCAL<br>TGAGTCGT                     | AC<br>TG                  |
| TTCCTTCTCC CGCC  |   | 180   | 190                                    | 2   | 00<br>*                   |
| 160<br>*<br>TCCTAGACGC TGG<br>AGGATCTGCG ACC             | 170<br>*<br>TAGAAAG T                             | *   | GAGCCTGCC.<br>CTCGGACGG                | A TCCAGTCO<br>T AGGTCAGO                  | etg<br>Cac                |
| AGGATCTGCG ACC   | ATCTTTC A   | 100.1-                                      | 2.4                                    | 10  | 250                       |
| 210  | 220   | 230   |  |   | •                         |
|  | *<br>TTGGGTC T<br>AAACCCAG A                      | GAAGTGTCT<br>CTTCACAGA                      | GTGAGACCT<br>CACTCTGG                  | TC ACAGAAG<br>AG TGTCTTC                  | TCG                       |
| GCACGTC110 000   |   | 280   |  | 90  | <b>*</b>                  |
| 260<br>*<br>ACCCCTGGGC TC<br>TGGGGACCCG AG               | 270<br>*<br>CACTTACC<br>GTGAATGG                  | TGCCCCTG<br>ACGGGGGAC                       | *<br>C TCCTTCAG<br>G AGGAAGTG          | GG ATGGAG<br>CCC TACCTC<br>MetGlu         |                           |
|  |   | 33  |  | 340                                       | 350<br>*                  |
| 310  | 320   | _   | *                                      | *<br>mcn ccggA                            | ACGTG                     |
| 310<br>*<br>TGGCGGCCAG C<br>ACCGCCGGTC G<br>MetAlaAlaSer | ACTTCCCTG<br>TGAAGGGAC                            | CCTGACCC'<br>GGACTGGG<br>ProAspPr           | IG GAGACTT<br>AC CTCTGAA<br>o GlyAspPh | ACT GGCCT<br>neAsp ArgA                   | TGCAC<br>snVal>           |
| MetAlaAlaSel   |   | 3   | 880                                    | 390                                       | 400<br>*                  |
| 360  | 370   |   | *                                      | *<br>************************************ | CTTCAA                    |
| 360<br>*<br>CCCCGGATCT<br>GGGGCCTAGA<br>ProArglle C      | GTGGGGTGT<br>CACCCCACA<br>ysGlyValC               | G TGGAGACO<br>C ACCTCTGO<br>YS GlyAsp       | CGA GCCACT<br>GCT CGGTGA<br>Arg AlaThi | CCGA AAGT                                 | GAAGTT<br>sPheAsn><br>450 |
|  | 4.0   |   | 430                                    | 1   |                           |
| 410<br>*<br>TGCTATGACC<br>ACGATACTGG<br>AlaMetThr        |   | * ccaaag                                    | TAbue ine                              | GGCGA AGCA<br>CCGCT TCG<br>ArgArg Ser     | 500                       |
|  |   | 70  | 480                                    |   | -                         |
| 466<br>GGAAGGCAC'<br>CCTTCCGTG<br>ArgLysAlaL             | r ATTCACC<br>A TAAGTGG<br>eu PheThr               | *<br>PGC CCCTTC<br>ACG GGGAAC<br>Cys ProPho | CAACG GGGA<br>STTGC CCCT<br>eAsn GlyAs | CTGCCG CAT<br>GACGGC GTA<br>pCysArg I     | AGTGGTTC<br>LeThrLys>     |

<del>WO 99/16872 -</del>

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| 510                       | 520                                     | 530                       | 540                       | 550                                      |
|---------------------------|---|---------------------------|---------------------------|--|
| GACAACCGAC<br>CTGTTGGCTG  | GCCACTGCCA<br>CGGTGACGGT                | GGCCTGCCGG<br>CCGGACGGCC  | CTCAAACGCT<br>GAGTTTGCGA  | GTGTGGACAT<br>CACACCTGTA                 |
| AspAsnArg                 | ArgHisCysGl                             | n AlaCysArg               | LeuLysArg                 | CysValAspIle>                            |
| 560<br>*                  | *                                       | 580<br>*                  | 590<br>*                  | 600<br>*                                 |
| GCCGTACTAC                | AAGGAGTTCA<br>TTCCTCAAGT                | AAGACTGTCT                | ACTCCTTCAC                | GTCTCCTTCG                               |
|                           | LysGluPhe :                             |                           |                           |  |
| 610                       | *                                       | 630<br>*                  | 640                       | 650<br>*                                 |
| CCCTCTACTA                | CCTGAAGCGG<br>GGACTTCGCC                | TTCCTCCTCC                | TCCGGAACTT                | GGACAGTCTG<br>CCTGTCAGAC<br>s AspSerLeu> |
| 660                       |   | 680                       | 690                       | 700                                      |
| *                         | *<br>TGTCTGAGGA                         | *                         | +                         | *  |
| GCCGGGTTCG                | ACAGACTCCT                              | CGTCGTCGCG                | TAGTAACGGT                | ATGACGACCT                               |
| 710                       |   |                           |                           | IleLeuLeuAsp>                            |
| *                         | *                                       | 730                       | 740                       | 750                                      |
| GCGGGTGGTA                | AAGACCTACG<br>TTCTGGATGC                | TGGGGTGGAT                | GAGGCTGAAG                | ACGGTCAAGG                               |
|                           | LysThrTyr I                             | AspProThrTy               | r SerAspPhe               | CysGlnPhe>                               |
| 760<br>*                  | *                                       | 780<br>*                  | 790<br>*                  | * 800                                    |
| CCGGAGGTCA                | TCGTGTGAAT<br>AGCACACTTA<br>1 ArgValAsn | CTACCACCTC                | CCTCGGTAGG                | TTCCAGGCCC<br>AAGGTCCGGG<br>o SerArgPro> |
| 810                       |   | 830                       | 840                       | 850                                      |
| AACTCCAGAC                | * ACACTCCCAG                            | *                         | *                         | *  |
| TTGAGGTCTG                | TGTGAGGGTC                              | GAAGAGACCC                | CTGAGGAGGA                | GGAGGACGAG<br>SerSerCysSer>              |
| 860                       |   | 880                       |                           | -  |
| *                         | *                                       | *                         | 890<br>*                  | 900                                      |
| TCTAGTGACA                | ATCACCTCTT<br>TAGTGGAGAA<br>IleThrSer   | GTCTGTACTA                | CCTGAGCAGG                | TCGAAGAGGT                               |
| 910                       | 920                                     | 930                       | 940                       | 950                                      |
| *<br>ATCTGGATCT           | *<br>GAGTGAAGAA                         | *<br>GATTCAGATG           | * ACCCTTCTGT              | *<br>GACCCTAGAG                          |
| TAGACCTAGA<br>AsnLeuAspLe | CTCACTTCTT<br>u SerGluGlu               | CTAAGTCTAC<br>AspSerAsp   | TGGGAAGACA<br>AspProSerVa | CTGGGATCTC<br>l ThrLeuGlu>               |
| 960                       |   | 980                       | 990                       | 1000                                     |
| CTGTCCCAGC                | *<br>TCTCCATGCT                         | * GCCCCACCTG              | * GCTGACCTGG              | *<br>TCAGTTACAG                          |
| GACAGGGTCG<br>LeuSerGln   | AGAGGTACGA<br>LeuSerMetLe               | CGGGGTGGAC<br>u ProHisLeu | CGACTGGACC<br>AlaAspLeu   | AGTCAATGTC<br>ValSerTyrSer>              |

₩<del>O 99/16872</del>

Title: "Isoforms of the Human Vitamin D.P. ceptor" Inventor: Linda Anne Crofts

Application No.: 09/509,482 Atty. Docket No. RICE-014

PCT/AU98/00817-

1050 1040 1030 1020 1010

CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

1100 1090 1080 1070 1060

TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

1150 1140 1130 1120 1110

ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

1190 1180 1170 1160

CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

1230 1220 1210

GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

1300 1290 1280 1270

AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

1340 1330 1320 1310

CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

1400 1390 1380 1370 1360

CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

1450 1440 1430 1420 1410

CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT GTGGGCGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

1490 1480 1470 1460

AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>

Title: "Isoforms of the Human Vitamin D Recept Inventor: Linda Anne Crofts Application No.: 09/509,482

Atty. Docket No. RICE-014

WO 99/16872

PCT/AU98/00817

1510

1540

1550

TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

1560

GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO: 7)
CACAAACCGT TACTCTAGAG GACT (SEQ ID NO: Zo)
ValPheGly AsnGluileSer \*\*\*>(SEQ ID NO: IZ)

WO 99/16872

Title: "Isoforms of the Human Vitamin D R Inventor: Linda Anne Crofts lication No : 09/509.482

| Inventor: Linda Anne Crofts  |                   |
|--|-------------------|
| Application No.: 09/509,482<br>Atty. Docket No. RICE-014   |                   |
| Atty. Docker No. Idob  | PCT/AU98/00817    |
| 4 -4   |                   |
| F1G. 5C  |                   |
| ·  | 900               |
| 870 880 890  | * *               |
| 860 870 * * * * *  | AMCCA A A AGG     |
| * * * * * * * * * * * * * * * * * * *  | TACGTTTTCC        |
| CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC GAGGTACGAC GACTGGACCA GTCAATGTCG GAGGTACGAC GACTGGACCA GTCAATGTCG GAGGTACGAC GAGGTACGAC GAGGTACGAC GAGGTACGAC GAGGTACGAC GAGGTACGAC GAGGTACGAC GACCTGGT CAGTTACAGC GAGGTACGAC GAGGTACGAC GACGTACGAC GACGTACGAC GACCTGGACCAG GACGTACGAC GACGTACAC GACCAC GACGTACAC GACCAC GA | TleGlnLys>        |
| GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG<br>GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG<br>GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG<br>SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer  | 1204              |
|  | 950               |
| 920 930  | . * *             |
| * * * *  | CACCTCTGAG        |
| TCATTGGCTT TGCTAAGATG ATACCAGGAT TCATTGGG  | GTGGAGACTC        |
| TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCA<br>AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA<br>VallleGlyPhe AlaLysMet IleProGly PheArgAspLo   | eu ThrSerGlu>     |
| VallleGlyPhe AlabyShee   | 1000              |
| 980  | • •               |
| 960 970 * * *  | *                 |
| GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTC   | A TCAIGIIGG       |
| GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTC CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAG CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAG   | TleMetLeuArg>     |
| GACCAGATCG TACTOCACG TAACTCACGC CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCACG CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCACG AspGlnIle ValLeuLeuLys SerSerAla IleGluVal   | L IICIII          |
| AspGINITE VALUE 1030 10  | 40 1050           |
| 1010 1020  | * * *             |
| * * * *  | CC TGTGGCAACC     |
| CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGA<br>GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCT<br>GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCT  | GG ACACCGTTGG     |
| GAGGTTACTC AGGAAGTGGT ACCIGCTON  | hr CysGlyAsn>     |
| SerAsnGlu SerFile  | 4400              |
| 1080   | )90 1100<br>* * * |
|  |                   |
| * * * * * * * * * * * * * * * * * * *  | CGG ACACAGGGAC    |

AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

1140 1130 1120 1110

GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

1200 1190 1180 1170 1160

CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

1250 1240 1230 1220

CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

1300 1290 1280 1270 1260

CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>

Title: "Isoforms of the Human Vitamin Inventor: Linda Anne Crofts

Application No.: 09/509,482 Atty. Docket No. RICE-014



WO 99/16872

PCT/AU98/00817

F1G. 5D

1310 1320 1330 1340 1350

GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

1360 1370 1380 1390 1400

GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

1410 1420 1430 1440 1450

CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

1460

TGAGATCTCC TGA (SEQ ID NO: 2)
ACTCTAGAGG ACT (SEQ ID NO: 17)
GlulleSer \*\*\*>(SEQ ID NO: 9)

PCT/AU98/00817

F19. 6A

TRANSCRIPT 9

(Sequence Range: 1 to 1382)

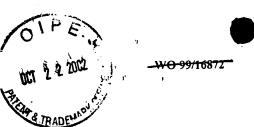
| Ç | inge: 1    | CO 1      | 302)    |       |         |                |         |             |          |          |
|---|------------|-----------|---------|-------|---------|----------------|---------|-------------|----------|----------|
|   |            | 10        |         | 20    |         | 30             |         | 40          |          | 50       |
|   | *          | *         | *       | *     | . *     | *              | *       | *           | *        | *        |
|   | GTTTCCT    | TCT       | TCTGTCG | GGG   | CGCCTT  | GGCA           | TGGAGT  | GGAG        | GAATAA   | GAAA     |
|   | CAAAGGA    |           |         |       |         |                |         |             |          |          |
|   |            |           |         |       |         |                |         |             | AsnLy    |          |
|   |            |           |         |       |         |                |         |             |          |          |
|   |            | 60        |         | 70    |         | 80             |         | 90          |          | 100      |
|   | *          | *         | *       | *     | *       | *              | *       | *           | *        | *        |
|   | AGGAGCG    |           |         |       |         |                |         |             |          |          |
|   |            |           | CCGACAC |       |         |                |         |             |          |          |
|   | ArgSerA    | sp 1      | rpLeuSe | erMet | : ValLe | uArg           | ThrAla  | GIY /       | algiug   | TAWEC>   |
|   |            | 110       |         | 120   |         | 130            |         | 140         |          | 150      |
|   | *          | *         | *       | 120   | *       | *              | *       | *           | *        | *        |
|   | GGAGGCA    | ATG       | GCGGCCZ | AGCA  | CTTCCC  | TGCC           | TGACCC  | TGGA        | GACTTT   | GACC     |
|   |            |           | CGCCGG  |       |         |                |         |             |          |          |
|   |            |           | AlaAlaS |       |         |                |         |             |          |          |
|   |            |           |         |       |         |                | -       | _           | _        |          |
|   |            | 160       |         | 170   |         | 180            |         | 190         |          | 200      |
|   | *          | *         | *       | *     | *       | *              | *       | *           | *        | *        |
|   |            |           | CCGGAT  |       |         |                |         |             |          |          |
|   |            |           | GGCCTA  |       |         |                |         |             |          |          |
| Ž | ArgAsnVa   | alPro     | ArgIle  | eCys  | GlyVal  | Cys (          | SlyAspA | rgAla       | a ThrGl  | yPhe>    |
|   |            | 210       |         | 220   | ·       | 220            |         | 240         |          | 250      |
|   |            | 210       | *       | 220   | *       | 230            | *       | 24U<br>*    | *        | 2JU<br>* |
|   | C y CmmC i |           | CTATGA  |       |         |                |         |             | TCAGGC   | GAAG     |
|   |            |           | GATACT  |       |         |                |         |             |          |          |
|   |            |           | AlaMetT |       |         |                |         |             |          |          |
|   |            |           |         | 0     |         | <b>J</b> - J - |         |             |          | •        |
|   |            | 260       |         | 270   |         | 280            |         | 290         |          | 300      |
|   | *          | *         | *       | *     | *       | *              | *       | *           | *        | *        |
|   |            |           | AAGGCA  |       |         |                |         |             |          |          |
|   |            |           | TTCCGT  |       |         |                |         |             |          |          |
|   | MetLy      | sArg      | LysAla  | Leu   | PheThrC | ysPr           | o PheAs | snGly       | AspCys   | Arg>     |
|   |            |           |         | 200   |         | 220            |         | 240         |          | 250      |
|   |            | 310       |         | 320   |         | 330            | *       | 340         | *        | 350<br>* |
|   | mozocz     | ^<br>2002 | CAACCG  |       | CACTICA |                |         | -ርረርርጥ<br>- | CAAACG   | ድርጥርጥ    |
|   |            |           | GTTGGC  |       |         |                |         |             |          |          |
|   | IleThrL    | veye      | n AsnAr | aAra  | HisCvs  | Gln            | AlaCvs  | AraLe       | u LvsAr  | aCvs>    |
|   | TTGIHLD    | , ond     | e nomi  | 3 3   |         |                |         |             | <i>y</i> | J-3      |
|   |            | 360       |         | 370   |         | 380            |         | 390         |          | 400      |
|   | *          | *         | *       | *     | *       | *              | *       | *           | *        | *        |
|   |            |           | GCATGA  |       |         |                |         |             |          |          |
|   |            |           | CGTACT  |       |         |                |         |             |          |          |
|   | ValAsp     | Ile       | GlyMetM | etLy  | s GluPh | ieIle          | LeuTh   | rAsp        | GluGlu\  | /alGln>  |
|   |            |           |         |       |         |                |         |             |          |          |

<del>WO-99/1687</del>2

Title: "Isoforms of the Human Vitamin D R Inventor: Linda Anne Crofts Application No.: 09/509,482 Atty. Docket No. RICE-014

PCT/AU98/00817

|              | -107        | 20-           |                          |               |
|--------------|-------------|---------------|--------------------------|---------------|
| 410          | 420         | 430           | 440                      | 450           |
| * *          | * *         | * *           | * *                      | * *           |
|              |             |               | GGAGGAGGAG               |               |
|              |             |               | CCTCCTCCTC  GluGluGlu    |               |
| ArgLysArg    | Glumetile i | Jeuryski Gry: | s GruGruGru              | Alabeubys>    |
|              |             |               |                          |               |
| 460          | 470         | 480           | 490                      | 500           |
| * *          | * *         | * *           | * *                      | * *           |
|              |             |               | AGCAGCGCAT               |               |
|              |             |               | TCGTCGCGTA               |               |
| AspSerLeuArg | g ProLysLeu | SerGruGru (   | JINGINATGII              | e llealaile>  |
|              |             |               |                          |               |
| 510          | 520         | 530           | 540                      | 550           |
| * *          | * *         | * *           | * *                      | * *           |
|              |             |               | CCCACCTACT               |               |
|              |             |               | GGGTGGATGA               |               |
| LeuLeuAsp A  | AlaHisHisPA | s ThriyrAsp   | Proffirlyr :             | SerAspPheCys> |
| 560          | 570         | 580           | 590                      | 600           |
| * *          | * *         | * *           | * *                      | * *           |
| CCAGTTCCGG   | CCTCCAGTTC  | GTGTGAATGA    | TGGTGGAGGG               | AGCCATCCTT    |
|              |             |               | ACCACCTCCC               |               |
| GlnPheArg    | ProProVal A | ArgValAsnAs   | p GlyGlyGly              | SerHisPro>    |
| 610          | 620         | 630           | 640                      | 650           |
| * *          | * *         | * *           | * *                      | * *           |
| CCAGGCCCAA   | CTCCAGACAC  | ACTCCCAGCT    | TCTCTGGGGA               | CTCCTCCTCC    |
|              |             |               | AGAGACCCCT               |               |
| SerArgProAs  | n SerArgHis | ThrProSer     | PheSerGlyAs              | p SerSerSer>  |
|              | 670         | 600           | 600                      | 700           |
| 660<br>* *   | 670<br>* *  | 680<br>* *    | 690<br>* *               | 700<br>* *    |
|              |             |               | GACATGATGG               | ACTCGTCCAG    |
|              |             |               | CTGTACTACC               |               |
| SerCysSer    | AspHisCysIl | e ThrSerSer   | AspMetMet .              | AspSerSerSer> |
|              |             |               |                          |               |
| 710          | 720<br>* *  | 730<br>* *    |                          | 750           |
| ~ ~ ×        |             |               | TTCAGATGAC               |               |
|              |             |               | AAGTCTACTG               |               |
|              |             |               | p SerAspAsp              |               |
|              | _           |               |                          |               |
| 760          | 770         |               |                          | 800           |
| * *          | * *         | * *           | * *                      | * *           |
|              |             |               | CCCACCTGGC<br>GGGTGGACCG |               |
|              |             |               |                          | a AspLeuVal>  |
|              |             |               |                          | •             |
| 810          |             |               |                          | 850           |
| * *          | * *         |               |                          | * *           |
|              |             |               | GCTAAGATGA<br>CGATTCTACT |               |
|              |             |               |                          | IleProGlyPhe> |
|              |             |               |                          |               |



PCT/AU98/00817-

| 860  | 870  | 880  | 890   | 900   |
|--|--|--|---|---|
| * *  | * *  | . * *  | * *   | * *   |
| CAGAGACCTC   | ACCTCTGAGG   | ACCAGATCGT   | ACTGCTGAAG  | <b>ТСАВСТСССА</b>   |
|  |  | TGGTCTAGCA   |   |   |
|  |  | AspGlnIleVal   |   |   |
| gnspbcu  | iniberoru .  | poznizio (a.   |   | 00100111147   |
| 910  | 920  | 930  | 940   | 950   |
| * *  | * *  | * *  | * *   | * *   |
| TTGAGGTCAT   | CATGTTGCGC   | TCCAATGAGT   | CCTTCACCAT  | GGACGACATG  |
|  |  | AGGTTACTCA   |   |   |
|  |  |  |   | t AspAspMet>  |
|  | _  |  |   |   |
| 960  | 970  | 980  | 990   | 1000  |
| * *  | * *  | * *  | * *   | * *   |
| TCCTGGACCT   | GTGGCAACCA   | AGACTACAAG   | TACCGCGTCA  | GTGACGTGAC  |
| AGGACCTGGA   | CACCGTTGGT   | TCTGATGTTC   | ATGGCGCAGT  | CACTGCACTG  |
| SerTrpThr (  | CysGlyAsnGl  | n AspTyrLys  | TyrArgVal   | SerAspValThr>   |
|  |  |  |   |   |
| 1010   | 1020   | 1030   | 1040  | 1050  |
| * *  | * *  | * *  | * * *   | * *   |
|  |  | AGCTGATTGA   |   |   |
|  |  | TCGACTAACT   |   |   |
| LysAlaGly  | HisSerLeu (  | GluLeuIleGlu   | ı ProLeuIle   | LysPheGln>  |
|  |  |  |   |   |
| 1060   | 1070   | 1080<br>* *  | 1090<br>* *   | 1100  |
|  |  |  |   |   |
|  |  | TTGCATGAGG   |   |   |
|  |  | AACGTACTCC   |   |   |
| vargrybeuby  | s LysLeuAsn  | LeumisGiu (  | stugiunisva   | l LeuLeuMet>  |
| 1110   | 1120   | 1130   | 1140  | 1150  |
| * *  | * *  | * *  | * *   | * *   |
| GCCATCTGCA   | ጥርርጥርጥርርር  | AGATCGTCCT   | GGGGTGCAGG  | ACGCCGCGCT  |
|  |  | TCTAGCAGGA   |   |   |
|  |  |  |   | AspAlaAlaLeu>   |
|  |  | <b>-</b>   |   |   |
| 1160   | 1170   | 1180   | 1190  | 1200  |
| * *  | * *  | * *  | * *   | * *   |
| CATTCACCCC   |  |  |   |   |
| GVIIGNOCC  |  | GCCTGTCCAA   |   | ACGTACATCC  |
|  | ATCCAGGACC   |  | CACACTGCAG  |   |
| CTAACTCCGG   | ATCCAGGACC<br>TAGGTCCTGG   | GCCTGTCCAA   | CACACTGCAG<br>GTGTGACGTC  | TGCATGTAGG  |
| CTAACTCCGG   | ATCCAGGACC<br>TAGGTCCTGG   | GCCTGTCCAA<br>CGGACAGGTT   | CACACTGCAG<br>GTGTGACGTC  | TGCATGTAGG  |
| CTAACTCCGG   | ATCCAGGACC<br>TAGGTCCTGG<br>IleGlnAsp  | GCCTGTCCAA<br>CGGACAGGTT<br>ArgLeuSerAsı<br>1230   | CACACTGCAG<br>GTGTGACGTC<br>n ThrLeuGln   | TGCATGTAGG<br>ThrTyrIle>  |
| CTAACTCCGG<br>IleGluAla<br>1210  | ATCCAGGACC TAGGTCCTGG IleGlnAsp 1220 *   | GCCTGTCCAA<br>CGGACAGGTT<br>ArgLeuSerAsı<br>1230<br>* *  | CACACTGCAG<br>GTGTGACGTC<br>n ThrLeuGln<br>1240<br>* *  | TGCATGTAGG ThrTyrIle>  1250 * *   |
| CTAACTCCGG IleGluAla 1210 * * GCTGCCGCCA   | ATCCAGGACC TAGGTCCTGG IleGlnAsp 1220 * * * * * * * *   | GCCTGTCCAA<br>CGGACAGGTT<br>ArgLeuSerAsı<br>1230<br>* *  | CACACTGCAG GTGTGACGTC ThrLeuGln 1240 * TGCTCTATGC   | TGCATGTAGG ThrTyrIle>  1250   |
| CTAACTCCGG IleGluAla 1210 * * GCTGCCGCCA CGACGGCGGT  | ATCCAGGACC TAGGTCCTGG IleGlnAsp  1220  * * CCCGCCCCCG GGGCGGGGC  | GCCTGTCCAA CGGACAGGTT ArgLeuSerAsı 1230 * * GGCAGCCACC CCGTCGGTGG  | CACACTGCAG GTGTGACGTC ThrLeuGln 1240 * * TGCTCTATGC ACGAGATACG  | TGCATGTAGG ThrTyrIle>  1250   |
| CTAACTCCGG IleGluAla 1210 * * GCTGCCGCCA CGACGGCGGT  | ATCCAGGACC TAGGTCCTGG IleGlnAsp  1220  * * CCCGCCCCCG GGGCGGGGC  | GCCTGTCCAA CGGACAGGTT ArgLeuSerAsı 1230 * * GGCAGCCACC CCGTCGGTGG  | CACACTGCAG GTGTGACGTC ThrLeuGln 1240 * * TGCTCTATGC ACGAGATACG  | TGCATGTAGG ThrTyrIle>  1250   |
| CTAACTCCGG IleGluAla  1210  * GCTGCCGCCA CGACGGCGGT ArgCysArgHi                                | ATCCAGGACC TAGGTCCTGG IleGlnAsp  1220  * CCCGCCCCCG GGGCGGGGCC S ProProPro                               | GCCTGTCCAA CGGACAGGTT ArgLeuSerAsı 1230  * * GGCAGCCACC CCGTCGGTGG GlySerHis                             | CACACTGCAG GTGTGACGTC ThrLeuGln 1240  * TGCTCTATGC ACGAGATACG LeuLeuTyrAl                                 | TGCATGTAGG ThrTyrIle>  1250  * * CAAGATGATC GTTCTACTAG a LysMetIle>                       |
| CTAACTCCGG IleGluAla  1210  * GCTGCCGCCA CGACGGCGGT ArgCysArgHi  1260                          | ATCCAGGACC TAGGTCCTGG IleGlnAsp  1220  * CCCGCCCCCG GGGCGGGGCS ProProPro                                 | GCCTGTCCAA CGGACAGGTT ArgLeuSerAsı 1230 * GGCAGCCACC CCGTCGGTGG GlySerHis                                | CACACTGCAG GTGTGACGTC ThrLeuGln 1240  * TGCTCTATGC ACGAGATACG LeuLeuTyrAl                                 | TGCATGTAGG ThrTyrIle>  1250  * * CAAGATGATC GTTCTACTAG a LysMetIle>  1300                 |
| CTAACTCCGG IleGluAla  1210  * GCTGCCGCCA CGACGGCGGT ArgCysArgHi  1260  *                       | ATCCAGGACC TAGGTCCTGG IleGlnAsp  1220  * * CCCGCCCCCG GGGCGGGGC s ProProPro  1270  * *                   | GCCTGTCCAA CGGACAGGTT ArgLeuSerAsı 1230 * GGCAGCCACC CCGTCGGTGG GlySerHis 1280 *                         | CACACTGCAG GTGTGACGTC ThrLeuGln  1240  * TGCTCTATGC ACGAGATACG LeuLeuTyrAl  1290  *                       | TGCATGTAGG ThrTyrIle>  1250  * * CAAGATGATC GTTCTACTAG a LysMetIle>  1300  * *            |
| CTAACTCCGG IleGluAla  1210  * GCTGCCGCCA CGACGGCGGT ArgCysArgHi  1260  * CAGAAGCTAG            | ATCCAGGACC TAGGTCCTGG IleGlnAsp  1220  * * CCCGCCCCCG GGGCGGGGC S ProProPro  1270  * CCGACCTGCG          | GCCTGTCCAA CGGACAGGTT ArgLeuSerAsı 1230 * * GGCAGCCACC CCGTCGGTGG GlySerHis 1280 * * CAGCCTCAAT          | CACACTGCAG GTGTGACGTC  1240  * TGCTCTATGC ACGAGATACG LeuLeuTyrAl  1290  * GAGGAGCACT                      | TGCATGTAGG ThrTyrIle>  1250  * * CAAGATGATC GTTCTACTAG a LysMetIle>  1300  * * CCAAGCAGTA |
| CTAACTCCGG IleGluAla  1210  * GCTGCCGCCA CGACGGCGGT ArgCysArgHi  1260  * CAGAAGCTAG GTCTTCGATC | ATCCAGGACC TAGGTCCTGG IleGlnAsp  1220  * CCCGCCCCCG GGGCGGGGC s ProProPro  1270  * CCGACCTGCG GGCTGGACGC | GCCTGTCCAA CGGACAGGTT ArgLeuSerAsi 1230  * GGCAGCCACC CCGTCGGTGG GlySerHis 1280  * CAGCCTCAAT GTCGGAGTTA | CACACTGCAG GTGTGACGTC ThrLeuGln  1240  * TGCTCTATGC ACGAGATACG LeuLeuTyrAl  1290  * GAGGAGCACT CTCCTCGTGA | TGCATGTAGG ThrTyrIle>  1250  * * CAAGATGATC GTTCTACTAG a LysMetIle>  1300  * *            |

WO 99/16872~

Title: "Isoforms of the Human Vitamin Inventor: Linda Anne Crofts Application No.: 09/509,482 Atty. Docket No. RICE-014

\*PCT/AU98/00817-

1310 1320 1330 1340

CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

1360

TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO: 3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO: 18)
ValLeuGluVal PheGlyAsn GluIleSer \*\*\*>(SEQ ID NO: 10)